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# ALIGNMENTS

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(first entry)

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Claim

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                                                                                                                       The present sequence is Pasteurella (Mannheimia) haemolytica modified leukotoxin-50 (lkt50) protein. The modification comprises the removal of amino acids within the hydrophobic transmembrane domain of a full length leukotoxin protein. Modified leukotoxin sequences are used in vaccines to treat or prevent diseases associated with leukotoxin, e.g., respiratory disease, and Mannheimia infection (particularly M. haemolytica infection). In addition, the vaccine
                                                                                                                                                                                                                                                                                                                                                        Claim 4; Fig 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Modified leukotoxin polypeptide is useful in a vaccine to prevent or treat Mannheimia (Pasteurella) infection (particularly M. haemolytica infection), and disease associated with a leukotoxin, e.g., respirato
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                                                                          used to prepare a medicament. Furthermore, the plant the modified leukotoxin sequences is fed to an animal sequences.
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                       The present sequence is Pasteurella (Mannheimia) haemolytica modified leukotoxin-66 (lkt66) protein. The modification comprises the removal of amino acids within the hydrophobic transmembrane domain of a full length leukotoxin protein. Modified leukotoxin sequences are used in vaccines to treat or prevent diseases associate with leukotoxin, e.g., respiratory disease, and Mannheimia infection (particularly M. haemolytica infection). In addition, the vaccine is used to prepare a medicament. Furthermore, the plant transformed with modified leukotoxin sequences is fed to an animal such as a with modified leukotoxin sequences, is fed to an animal such as a
                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified leukotoxin polypeptide is useful in a vaccine to pitreat Mannheimia (Pasteurella) infection (particularly M. hi infection), and disease associated with a leukotoxin, e.g.,
                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                         disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                animal feed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leukotoxin 66; lkt66; respiratory disease; infection; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pasteurella haemolytica modified leukotoxin 66 (lkt66) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE04636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE04636 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYGU-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-DEC-2000; 2000WO-CA01498
 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lmmunostimulant; antibacterial;
                                   1 FLSELNKELEAE
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fllnlnkelgae
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                                                                      Similarity
9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAD08975.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UNIV GUELPH OFFICE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shewen PE,
                                                                                                                                                                                            to prevent or treat respiratory diseases.
                                                                                                                                                            803
                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                  2; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mutant;
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                                                                                                                                                            AA;
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75.0%;
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75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lee RWH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         808
                                                                                    Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 23;
1; Mismatches
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                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vaccine;
                                                                                    DB
33;
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23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strommer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2
                                                                                                   Length 608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 450;
                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                    o prevent or haemolytica g., respiratory
                                                                                                                                                                                                                                                                               associated
                                                                  0;
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                                                                .Gaps
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XX LKT;
XX CA20
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AAR42385
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Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmid pAA352 is derived from pAA114, a clone isolated from a genomic library of p. haemolytica. The protein, designated "new leukotoxin" or "LKT 352" is 98% homologous to authentic leukotoxin. LKT 352 and pref. antigenic fragments of it, can be used in vaccines to protect cattle from respiratory diseases. They can also be used to produce antibodies for immunoaffinity purificn. of further proteins. [Fig. contg. sequence v. poor]. See also AAR10890, AAR10909, AAR10910 and AAQ10783.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1991-000097/01.
N-PSDB; AAQ10272.
                                                                                             Haemophilus somnus; immunogenic; haemolysin; LppB; LppC; thromboembolic meningoencephalitis; septicaemia; arthritis; pneumonia; lktA gene; haemin-binding protein; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 13; Fig 5; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e.g. pneumonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pasteurella haemolytica proteins vaccines to protect animals esp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Acres
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-APR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CA2014033-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR10889;
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  WO9321323-A
                                                 Pasteurella haemolytica.
                                                                                                                                                                                                        Recombinant leukotoxin peptide
                                                                                                                                                                                                                                                               19-APR-1994
                                                                                                                                                                                                                                                                                                                                                                    AAR42385 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYSA-) UNIV SASKATCHEWAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LKT; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leukotoxin 352 encoded by plasmid pAA352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-APR-1991
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9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            924 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Babiuk LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      haemolytica Al strain B122.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89US-0335018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90CA-2014033
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75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Potter AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       respiratory disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 43; DB Pred. No. 52; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        924
                                                                                                                                                                                                                                                                                                                                                                       924 AA
                                                                                                                                                                                                           from plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and genes - used for producing cattle from respiratory diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lawman MJP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          shipping fever pneumonia
                                                                                                                                                                                                           pCRR28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 924;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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RESULT
AAR42380
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Best Local S
Matches 9
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04-JUN-1992;
04-JUN-1992;
29-MAR-1993;
29-MAR-1993;
29-MAR-1993;
04-JUN-1992;
04-JUN-1992;
29-MAR-1993;
29-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The lppB gene protein was expressed in E. coli as a fusion to the Pasteurella haemolytica leukotoxin gene lkth coded for by plasmid pAA352. The llpB gene fragment was taken from pMS11. LppB can be used in vaccines for preventing or treating H. somnus infections, which cause thromboombolic meningo-encephalitis, septicaemia, arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haemophilus somnus immunogenic proteins used in vaccines selected from haemin-binding protein, haemolysin, LppB and corresp. DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
                                                                                         09-APR-1992;
                                                                                                                                          05-APR-1993;
                                                                                                                                                                                     28-OCT-1993
                                                                                                                                                                                                                                 W09321323-A
                                                                                                                                                                                                                                                                               Pasteurella
                                                                                                                                                                                                                                                                                                                        Haemophilus somnus; immunogenic; haemolysin; LppB; LppC; thromboembolic meningoencephalitis; septicaemia; arthritis; pneumonia; lktA gene; haemin-binding protein; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR42380 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 11; 119pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Harland RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-APR-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rioux C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 FLSELNKELEAE 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pneumonia in vertebrates. also AAR42370-86.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1993-351733/44.
DB; AAQ51086.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 || |||||:||
fllnlnkelqae 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               924
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                                                                                                                                                                                                                                                                               haemolytica
                                                                                                                                                                                                                                                                                                                                                                                                                     leukotoxin peptide (split) from plasmid pGCH4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfeiffer CG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SASKATCHEWAN
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93US-0038288.
93US-0038719.
                     92US-0865050.
92US-0893424.
92US-0893426.
93US-0038287.
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                                                                                                                                          93WO-CA00135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75.48;
75.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pontarollo RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 924
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and LppC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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0

-0038288

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RESULT

ARAF42378

ID ARAF4

XX ARAF4

AC ARAF4

XX HAEN

DT 19-2

DZ RECC

XX HAEN

KW HAEN

KW CHIC

XX PAST

XX WO9:1

PN WO9:1

PP 05-1

XX WO9:1

PR 04-,

PR 04-,

PR 29-1

PR 39-1

PR 39-1

PR 39-1

PR 4-1

PR 4-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                          04-JUN-1992;
04-JUN-1992;
29-MAR-1993;
29-MAR-1993;
29-MAR-1993;
WPI; 1993-351733/44
                                 Harland RJ, Pici
                                                                                                                    (UYSA-)
                                                                                                                                                                                                                                                                     09-APR-1992;
                                                                                                                                                                                                                                                                                                               05-APR-1993;
                                                                                                                                                                                                                                                                                                                                                          28-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                  W09321323-A
                                                                                                                                                                                                                                                                                                                                                                                                                                          Pasteurella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pneumonia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thromboembolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR42378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR42378 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The hmb gene encoding the haemin-binding protein was expressed in E. coli as a fusion to the Pasteurella haemolytica leukotoxin gene 1ktA coded for by plasmid pAA352. The hmb gene fragment was taken from pRAP504 and starts at the codon for the 33 rd amino acid residuals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haemophilus somnus immunogenic proteins used in vaccines selected from haemin-binding protein, haemolysin, LppB an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of ORF1. The haemin binding protein can be used in vaccines for preventing or treating H. somnus infections, which cause thromboembolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vertebrates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 meningo-encephalitis, septicaemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1993-351733/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Harland RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYSA-) UNIV SASKATCHEWAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 FLSELNKELEAE 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   corresp. DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fllnlnkelqae 435
                                                                                                                 UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 75.0%;
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ51082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR42370-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lktA gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Theisen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             somnus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   leukotoxin peptide (split) from plasmid pGCH5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fig 6;
                                                                                                                 SASKATCHEWAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfeiffer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mnus; immunogenic; haemolysin; Lpp
meningoencephalitis; septicaemia;
                                                                                                                                                       93US-0038288
93US-0038719
                                                                                                                                                                                                  92US-0893426
93US-0038287
                                                                                                                                                                                                                                            92US-0865050
92US-0893424
                                                                                                                                                                                                                                                                                                             93WO-CA00135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93US-0038719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein; 924
                                                                   cg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            haemin-binding protein; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
                                                                     Pontarollo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pontarollo RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 infections,
a, arthritis
                                                                     RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB
52;
                                                                     Potter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Potter AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LppB; LppC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and pneumonia in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 924;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LppB and LppC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR14482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                 pAA179. From this, two constructs were made in the ptac-based vector, pGH432:lacI digested with SmaI. One, pAA342, consisted the entire MaeI fragment from lktA while the other, pAA345, contained the entire MaeI fragment. Clone nAA347
                                                                                                                                                             Vaccines for Pasteurella haemolytica infection in cattle -comprise sub-unit antigens from P haemolytica fimbrial protein, plasmin receptor, 50 K outer membrane protein and leukotoxin.
                                                            to the same position on gels. The LKT352 gene was prepd. as follows: lkth, contg. the gene was ligated into the SmaI sippAA179. From this, two constructs were made
                                                                                                          LKT352 is 98% homologous with authentic leukotoxin and migrates
                                                                                                                                      Disclosure; Fig 5; 92pp; English.
                                                                                                                                                                                                                    WPI; 1991-324967/44.
                                                                                                                                                                                                                                                 Acres
                                                                                                                                                                                                                                                                                                 05-APR-1990;
                                                                                                                                                                                                                                                                                                                         17-OCT-1991;
                                                                                                                                                                                                                                                                                                                                                   17-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                           W09115237-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The hmb gene encoding the haemin-binding protein was expressed in E. coli as a fusion to the Pasteurella haemolytica leukotoxin gene lkth coded for by plasmid pAA352. The hmb gene fragment was taken from pRAP501 and starts at the codon for the third amino acid residue of ORP1. The haemin binding protein can be used in vaccines for preventing or treating H. somnus infections, which cause thromboembolic
                                                                                                                                                                                                                                                                     (UYSA-) UNIV SASKATCHEWAN
                                                                                                                                                                                                                                                                                                                                                                                                     Pasteurella
                                                                                                                                                                                                                                                                                                                                                                                                                          Antigen; leukotoxin; vaccine; lktA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LKT352.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR14482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR14482 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haemophilus somnus immunogenic proteins used in vaccines - selected from haemin-binding protein, haemolysin, LppB and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     See also AAR42370-86.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 5; 119pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vertebrates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           meningo-encephalitis, septicaemia, arthritis and pneumonia in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAQ51081.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FLSELNKELEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           corresp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fllnlnkelqae
                                                                                                                                                                                                                                               SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
9; Conser
            peptide
                                                                                                                                                                                                                                              Bariuk LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             924 AA;
                                                                                                                                                                                                                                                                                                                                                                                                   haemolytica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                              90US-0504850
            fragment.
ide at hig
                                                                                                                                                                                                                                                                                                                        91WO-CA00170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein; 926 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75.4%;
75.0%;
                                                                                                                                                                                                                                            Potter
Clone pAA342 expressed a truncated levels while pAA345 expressed full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
Pred.
                                                                                                                                                                                                                                            ĂĀ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                            Lawman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43;
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB
52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 924;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                             consisted of
                                                                        form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lppc,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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0;

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RESULT
AAR34545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
           and that had been boosted with a conc. culture supernatant of P. haemolytica to increase anti-leukotoxin antibody levels. Positive colonies were screened for their ability to produce leukotoxin by incubating cell lysates with bovine neutrophils and measuring the release of lactate dehydrogenase from the neutrophils. A 4kb fragment was obtd. Progressively larger clones were isolated by chromosome walking to isolate full length recombinants of ca. 8kb,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                length leukotoxin at very low levels. The 3' end of the lktA gene of pAA345 was therefore ligated to StyI/BamHI digested pAA342 to yield pAA352 contg. the LKT352 sequence. The protein expressed from the vector can be used to prepare a subunit vaccine with other P. haemolytica antigens, e.g. fimbrial protein, plasmin receptor or 50K outer membrane protein. The vaccines can be used to protect cattle from respiratory diseases such as pneumonia, esp.
                                                                                                                    Gene libraries of P. haemolytica Al (strain B122) were constructed in lambda gtll and pUCl3. Resulting clones were used to transform E coli and individual colonies were pooled and screened for reaction with serum from a calf which had survived a P. haemolytica infection
                                                                                                                                                                                                                             Immunological carrier system with enhanced immunogenicity comprises chimeric protein comprising leuco:toxin peptide homologous protein fused to antigen esp. somatostatin or gonadotropin releasing hormone
                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-1991;
14-OCT-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vector; LKT 352; flanking; recombinant; antigen; somatostatin; gonadotropin releasing hormone; rotavirus viral protein 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR34545;
                                                                                                                                                                                                   Disclosure;
                                                                                                                                                                                                                                                                                                            N-PSDB; AAQ41317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pasteurella haemolytica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            carrier protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Leukotoxin 352 produced from pAA352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR34545 standard; Protein; 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      shipping fever pneumonia.
See also AAR14481, 83,84 and 85.
                                                                                                                                                                                                                                                                                                                                                        Hughes HPA,
                                                                                                                                                                                                                                                                                                                                                                                        (UYSA-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-OCT-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            424 filminkelgae 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 FLSELNKELEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ø
                                                                                                                                                                                                                                                                                                                            1993-152482/18.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         926 AA;
The clone was subjected to
                                                                                                                                                                                                 Fig 3; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                         Potter AA,
                                                                                                                                                                                                                                                                                                                                                                                        SASKATCHEWAN
                                                                                                                                                                                                                                                                                                                                                                                                                     91US-0779171.
92US-0960932.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92WO-CA00449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lactation; reproduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75
75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . 08;
                                                                                                                                                                                                                                                                                                                                                         Redmond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB
. 52;
restriction enzyme digestion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                               or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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RESULT
AAR50291
Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       high levels and the other expressing the full length leukotoxin at low levels. The 3' end of the lktA gene from the full length clone was ligated to the truncated gene clone to yield plasmid pAA352. The clone was used to produce chimeric proteins by gene fusion with an antigen coding sequence, e.g. the coding sequence of somatostatin, gonadotrophin releasing hormone or rotavirus viral protein 4, i.e. leukotoxin works as a carrier protein to bring about a larger leukotoxin works as a carrier protein to bring about a larger leukotoxin works as a carrier protein to bring about a larger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immune response than the antigen alone. Immunisation with the antigens can regulate growth rate, lactation and reproductive efficiency. See also AAR34546-8.
                                                                                                                                                                               Haemophilus somnus outer membrane protein extract enriched with iron-regulated proteins, opt. contg leuco:toxin antigens, for use as vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vaccine; outer iron regulated
                                                                                                                                                           Claim 5; Fig
                                                                                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                                                                        Harland RJ,
                                                                                                                                                                                                                                                                                               (UYSA-) UNIV SASKATCHEWAN
                                                                                                                                                                                                                                                                                                                         02-JUL-1992;
                                                                                                                                                                                                                                                                                                                                                  29-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                           03-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                    CA2099707-A
                                                                                                                                                                                                                                                                                                                                                                                                                           Pasteurella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-0CT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR50291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR50291 standard; Protein; 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to yield two clones, one expressing truncated leukotoxin peptide at high levels and the other expressing the full length leukotoxin at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        424 filninkelgae 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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                                                                                                                                                                                                                                               1994-092909/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
9; Conserv
                                                                                                                                                                                                                                     AAQ44760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        926 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                          haemolytica Al (strain B122)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    leukotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                         5; 78pp; English
                                                                                                                                                                                                                                                                        Potter AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             membrane protein; OMP; Haemophilu protein; leukotoxin; Pasteurella
                                                                                                                                                                                                                                                                                                                         92US-0908253
                                                                                                                                                                                                                                                                                                                                                 93CA-2099707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75.4%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plasmid pAA352.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OMP; Haemophilus somnus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 haemolytica;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 926;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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A vaccine comprising an outer membrane protein (OMP) extract of Haemophilus somnus enriched with iron regulated proteins is new. The vaccine pref. further comprises an immunogenic leukotoxin polypeptide, esp. an immunogenic Pasteurella haemolytica leukotox homologous to LKT352. Example 1.2 describes the prodn. of P. haemolytica recombinant leukotoxin from pAA352. Two expression constructs were made. One, pAA342, contained the 5'-AhAII fragment of the ltkA gene, while the other, pAA345, contained the entire lktA gene. pAA342 expressed a truncated leukotoxin at very low levels, while pAA345 expressed full length leukotoxin at very low levels. Therefore, the 3' end of the ltkA gene pAA345 expressed full length leukotoxin at very low levels. Therefore, the 3' end of the levels paragraphy and the pAA345 expressed full length leukotoxin at very low levels.

leukotoxin

length of the

1ktA gene was ligated into pAA342,

yielding plasmid pAA352.

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₽ Qy
                                                                                                                                                                                                                                                                                               RESULT 11
AAW03945
ID AAW039
XX AAW039
XX Leukot
DT 20-NOV
XX Leukot
KW fusion
KW contra
XX W09624
XX W09624
XX UFSA-
XX W09624
XX W09624
XX W09624
XX UFSA-
XX UFSA-
XX UFSA-
XX WPI; 1
DR N-PSDB
XX WPI; 1
D
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                                                                                                                 Matches
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Best Local :
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Best Local :
Ļ
                                                                                                                                                                                                                                                                                                                                                                                          A truncated leukotoxin (AAW03945), LKT 352, lacks the cytotoxic portion of the native protein from Pasteurella haemolytica. It the product of plasmid pAA352 which carries a truncated lktA gen (AAT37179). A fusion protein (AAW03942) between LKT352 and a gonadotropin releasing hormone tetramer can be expressed in Escherichia coli. This is useful as a vaccine for fertility control, partic. immunological sterilisation of domestic or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Fig 3A-3I; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gonadotropin-releasing hormone multimer fusion proteins - w. Leukotoxin polypeptide for increased immunogenicity, useful antifertility vaccine prodn.
                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                       farm animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Manns JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYSA-) UNIV SASKATCHEWAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pasteurella haemolytica Al strain B122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09624675-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contraceptive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P. haemolytica truncated leukotoxin (LKT352).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW03945;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW03945 standard; Protein; 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     leukotoxin.

NB: the protein sequence however this protein is compared to the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fusion protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leukotoxin; LKT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                || |||||:||
424 fllnlnkelgae 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LKT352 or new leukotoxin
                                                 ш
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity tes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 FLSELNKELEAE 12
   FLSELNKELEAE 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1996-384447/38.
                                                                                                             Similarity 75.09; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Potter AA;
                                                                                                                                                                                                                                                                                               926 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          926 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; immunogen; vac
sterilisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95US-0387156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gonadotropin-releasing hormone; GnRH; immunogen; vaccine; fertility control; terilisation; plasmid pAA352.
                                                                                                                                           75.4%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75.4%;
75.0%;
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described
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                                                                                                                                           Score 43; DB
Pred. No. 52;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98% homologous to authentic
                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     comprises 926 amino acids, in the text as having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
. 52;
                                                                                                                                                                             17;
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                                                                                                      2;
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                                                                                                                                                                             Length 926;
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                                                                                                         Indels
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                                                                                                      0;
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                                                                                                      Gaps
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RESULT 13
AAR34547
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                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                     Matches
                                                                                                                                                                                                                                                              The present sequence represents a recombinantly produced or chemically synthesised leukotoxin 352 (LKT 352)polypeptide, derived from the lktA gene that is present in the plasmid pAA352. This gene produces a truncated protein that has an estimated molecular weight of about 99 kDa and lacks the cytotoxic portion of the molecule. Thus this gene has a higher expression level than that of the full-length molecule. This can be used in the construction of a chimeric protein that comprises a leukotoxin polypeptide, several multimers, and a GnRH sequence. The
                                  AAR34547 standard;
                                                                                                                                                                                                                                                  leukotoxin polypeptide, several multimers, and a GnRH sequence. The chimeric protein can be used as a vaccine to help reduce the incidence of
                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric protein of leukotoxin and gonadotropin releasing useful for, e.g. preparation of vaccines for reduction of of mammary tumours in mammals
                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                          mammary tumours in a mammalian individual
                                                                                                                                                                                                                                                                                                                                                                                 Claim 7; Figure 3.1-9; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-159540/14.
N-PSDB; AAV61530.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gonadotropin releasing hormone; GnHR; multimer; vaccine; tumour; Leukotoxin
                                                                                                424 fllnlnkelgae 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Manns JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYSA-) UNIV SASKATCHEWAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leukotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW79568;
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                                                                                                                          1 FLSELNKELEAE 12
                                                                                                                                                   Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Potter AA;
                                                                                                                                                                                                                   926 AA;
                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96US-0694865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97WO-CA00559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers 11..924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note=
                                    Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sing hormone; GnHR; chimera; leukotoxin polypeptide;
tumour; Leukotoxin 352; LKT 352; lkta; plasmid paa352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein; 926
                                                                                                                                                              75.4%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Recombinant leukotoxin peptide"
                                  936
                                                                                                                                                              Score 43;
Pred. No.
                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ã
                                                                                                                                                              DB
52;
                                                                                                                                                                          19;
                                                                                                                                                 2;
                                                                                                                                                                          Length 926;
                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       hormone
incidence
                                                                                                                                                 0,
                                                                                                                                                 Gaps
                                                                                                                                                 0;
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AAR34547

23-AUG-1993

(first entry)

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AAR34546
ID AAR3
XX
AC AAR3
XX
DT 23-4
XX
Some
                                                                          RESULT
                                                                                                    В
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                                                                                                                                                                                     Query Match
                                                                                                                                                                                                   releasing hormone (GnRH) gene were constructed on a Pharmacia Gene Assembler using standard phosporamidite chemistry. The oligonucleotides were annealed and ligated into vector pAA352 (contg. the Pateurella heamolytica leuko-toxin gene) which had been digested with BamHI. The ligated DNA was used to transform E. coli strain MH3000. Transformants contg. the oligonucleotide inserts were identified by restiction endonuclease mapping and the recombinant plasmid designated pAA502. The chimeric protein produced from the plasmid works to bring about a larger immune response than the antigen alone, i.e. the leukotoxin works as a carrier protein.
                                                                                                                                                                                                                                                                                                                                           Immunological carrier system with enhanced immunogenicity comprises chimeric protein comprising leuco:toxin peptide homologous protein fused to antigen esp. somatostatin or gonadotropin releasing hormone
Somatostatin-leukotoxin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-1991;
14-OCT-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vector; LKT 352; flanking; recombinant; antigen; somatos gonadotropin releasing hormone; rotavirus viral protein carrier protein; lactation; reproduction; SRIF.
                    23-AUG-1993
                                                        AAR34546 standard;
                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                       Oligonucleotides contg. sequences from bovine
                                                                                                                                                                                                                                                                                                                          Example 2; Fig 8; 95pp;
                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAQ41322
                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1993-152482/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09308290-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GnRH-leukotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYSA-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-OCT-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             кeу
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein
                                                                                                    || |||||:||
424 flln1nkelgae 435
                                                                          14
                                                                                                                                        Local Similarity hes 9; Conserv
                                                                                                                      1 FLSELNKELEAE 12
                                                                                                                                                                                                                                                                                                                                                                                                                     HPA,
                                                                                                                                                                                     936 AA;
                                                                                                                                        Conservative
                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                     Potter AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                      SASKATCHEWAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                       91US-0779171
92US-0960932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92WO-CA00449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "recombinant 927..936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "GnRH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  flanking;
                                                        Protein;
                                                                                                                                                75.4%;
                                                                                                                                                                                                                                                                                                                          English.
                                                                                                                                                                                                                                                                                                                                                                                                                     Redmond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prod
                                                        943
                                                                                                                                               Score 43;
Pred. No.
 fusion
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                                                                                                                                                                                                                                                                                                                                                                                                                     M
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                                                                                                                                               52;
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                                                                                                                                                          14;
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                                                                                                                                                                                                                                                                                                        gonadotrophin
                                                                                                                                                        Length 936;
                                                                                                                                        Indels
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Or
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                                                                                                                                       Gaps
                                                                                                                                        0;
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AAR34548
ID AAR3
XX
AC AAR3
XX
AC AAR3
XX
DT 23-A
DT 23-B
CX
XX
Vect
KW Vect
KW gona
                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       phosporamidite chemistry. The oligonucleotides were annealed and ligated into vector pAA352 (contg. the Pateurella heamolytica leukotoxin gene) which had been digested with BamHI. The ligated DNA was used to transform E. coli strain JM105. Transformants contg. the oligonucleotide inserts were identified by restiction endonuclease mapping and the recombinant plasmid designated pAA496. The chimeric protein produced from the plasmid works to bring about a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunological carrier system with enhanced immunogenicity comprises chimeric protein comprising leuco:toxin peptide homologous protein fused to antigen esp. somatostatin or gonadotropin releasing hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vector; LKT 352; flanking; recombinant; antigen; somatostatin; gonadotropin releasing hormone; rotavirus viral protein 4; carrier protein; lactation; reproduction; SRIF.
Vector; LKT 352; flanking; recombinant; antigen; somatostatin;
gonadotropin releasing hormone; rotavirus viral protein 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotides contg. sequences from bovine somatostatin (SRIF) gene were constructed on a Pharmacia Gene Assembler using standard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-1991;
14-OCT-1992;
                                                                 Rotavirus VP4-leukotoxin
                                                                                                                                                      AAR34548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             larger immune response than the antigen alone, i.e. the leukotoxin works as a carrier protein. See also AAR34545-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hughes HPA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-OCT-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
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                                                                                                            23-AUG-1993
                                                                                                                                                                                             AAR34548 standard; Protein; 951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Fig 6; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1993-152482/18.
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                                                                                                                                                                                                                                                                                                   424 filninkelgae 435
                                                                                                                                                                                                                                      15
                                                                                                                                                                                                                                                                                                                                        1 FLSELNKELEAE 12
                                                                                                                                                                                                                                                                                                                                                                                 Similarity 75.0
9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          943 AA;
                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Potter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SASKATCHEWAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91US-0779171.
92US-0960932.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "recombinant leukotoxin protein"
930..943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA,
                                                                                                                                                                                                                                                                                                                                                                                                     75.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "SRIF"
                                                               gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Redmond MJ;
                                                                                                                                                                                                                                                                                                                                                                                                   Score 43; DB
Pred. No. 53;
                                                                 fusion
                                                                                                                                                                                             AA.
                                                                 prod
                                                                                                                                                                                                                                                                                                                                                                                                                           14;
                                                                                                                                                                                                                                                                                                                                                                                    2
                                                                                                                                                                                                                                                                                                                                                                                                                         Length 943;
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Search completed: September 11, 2002, 08:58:48 Job time: 192 sec
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                                                                                                                         Query Match
Best Local Similarity
Matches 9; Conserva
                                                                                                                                                                                                                                 Oligonucleotides contg. sequences from bovine Rotavirus viral protein 4 (VP-4) gene were constructed on a pharmacia Gene Assembler using standard phosporamidite chemistry. The oligonucleotides were annealed and ligated into vector paA352 (contg. the Pateurella heamolytica leuko-toxin gene) which had been digested with BamHI. The ligated DNA was used to transform E. coli strain MH3000. Transformants contg. the oligonucleotide inserts were identified by restiction endonuclease mapping and the recombinant plasmid designated paA501. The chimeric protein produced from the plasmid works to bring about a larger immune response than the antigen alone, i.e. the leukotoxin works as a carrier protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunological carrier system with enhanced immunogenicity - comprises chimeric protein comprising leuco:toxin peptide or homologous protein fused to antigen esp. somatostatin or gonadotropin releasing hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-1991;
14-OCT-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1993-152482/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hughes HPA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-APR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                      424
                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                             See also AAR34545-7
                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Fig 8; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAQ41322.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYSA-) UNIV SASKATCHEWAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-OCT-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        carrier protein; lactation; reproduction; SRIF.
                                                                   1 FLSELNKELEAE 12
|| |||||:||
24 flln1nkelqae 435
                                                                                                                                                                                                  951 AA;
                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Potter AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91US-0779171.
92US-0960932.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92WO-CA00449.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "recombinant leukotoxin protein"
927..951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Rotavirus VP-4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1..926
                                                                                                                                         75.4%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Redmond MJ;
                                                                                                                            Score 43; DB Pred. No. 53; 1; Mismatches
                                                                                                                                                        DB 14; Length 951;
                                                                                                                            2;
                                                                                                                            Indels
                                                                                                                            0;
                                                                                                                          Gaps
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Database
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Maximum DB seq length: 2000000000
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                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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4646
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Copyright (c) 1993 - 2000 Comp
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# Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

14 806 17.3 15 434 9.3	806 17. 434 9. 432.5 9. 416 9.	432.5 9. 416 9. 410 8.	432.5 9.411 8.411 8.410 8.410 8.3.5 8.315	432.5 9. 411 8. 410 8. 433.5 8. 383.8 8.	432.5 9. 416 9. 411 8. 403.5 8. 391 8. 383 8.	432.5 9. 416 9. 411 8. 410 8. 403.5 8. 383 8. 383 7.	432.5 9. 432.5 9. 411 8. 410 8. 410 8. 301 8. 383 7. 343 7.	432.5 9. 416 9. 411 8. 410 8. 391 8. 393 8. 383 7. 332.5 7.	432.5 9. 432.5 9. 416 9. 411 8. 410 8. 403.5 8. 391 8. 393 8. 365 7. 332.5 7.	432.5 9. 432.5 9. 411 8. 410 8. 403.5 8. 303.5 8. 383 7. 332.5 7. 332.5 7.	432.5 9. 416 9. 411 8. 411 8. 411 8. 411 8. 413 8. 391 8. 393 8. 383 7. 343 7. 343 7. 332.5 7. 332.5 7. 332.5 7.	432.5 9. 411 8. 410 8. 411 8. 410 8. 391 8. 383 7. 332.5 7. 332.5 7.
	1705 1706 1829 1829 1302	1705 1706 1829 1829 1302 1208	1705 1706 1829 1829 1302 1302 1308 11363 11115	1705 1705 1829 1829 1302 1302 1308 1108 1115 2064	1705 1706 1829 1829 1302 1208 11208 11208 11115 2064	1705 1706 1829 1829 1302 1308 11308 11208 11208 11115 2064 2064	1706 1706 1829 1829 1302 1308 1108 1636 1115 2064 2084 2084 2084 2084 2084 2084 2084	1705 1706 11706 11829 11829 11302 11208 11208 11364 1115 2064 208 697 4936	1705 1829 1829 1829 1302 1302 1302 1308 1636 2064 2064 2064 2064 2064 2064 2064 206	1705 1706 1829 1829 1302 1302 1302 1306 1636 2064 2064 2084 2084 2084 2084 2084 2084 2084 208	1705 1706 1829 1829 1302 1302 1108 1108 11136 11136 2064 2064 2064 207 208 4936 1944	1705 1706 1829 1829 1302 1302 1302 1302 1302 1306 1636 1636 1636 1044 4936 1944 1944 1944 1944
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cytotoxin RTX homo		cytotoxin RTX homo iron-regulated pro iron-regulated pro hemolysin-type cal hemolysin-type cal	cytotoxin RTX homo iron-regulated pro iron-regulated pro hemolysin-type cal hemolysin-type cal hemolysin-type cal Fe-regulated RTX c	cytotoxin RTX homo iron-regulated pro iron-regulated pro hemolysin-type cal hemolysin-type cal Fe-regulated RTX c bacteriocin XF2407	cytotoxin RTX homo iron-regulated pro iron-regulated pro iron-regulated pro hemolysin-type cal hemolysin-type cal hemolysin-type cal hemolysin-type cal fe-regulated RTX c bacteriocin XF2407 leukotoxin A - Pas	cytotoxin RTX homo iron-regulated pro iron-regulated pro iron-regulated pro hemolysin-type cal hemolysin-type cal hemolysin-type cal ce-regulated RTX c bacteriocin XF2407 leukotoxin A - Pas probable RTX-famil	cytotoxin RTX homo iron-regulated pro iron-regulated pro hemolysin-type cal hemolysin-type cal fe-regulated RTX c bacteriocin XF2407 backeriocin A Pas probable RTX-famil hypothetical prote	cytotoxin RTX homo iron-regulated pro iron-regulated pro iron-regulated pro hemolysin-type cal hypothetical prote rhizobiocin/RTX to	cytotoxin RTX homo iron-regulated pro iron-regulated pro iron-regulated pro hemolysin-type cal hemolysin-type cal Fe-regulated RTX c bacteriocin XF2407 leukotoxin A - Pas probable RTX-famil hypothetical prote rhizobiocin/RTX to probable phosphoes	cytotoxin RTX homo iron-regulated pro iron-regulated pro iron-regulated pro hemolysin-type cal hemolysin-type cal hemolysin-type cal Fe-regulated RTX c bacteriocin XF2407 leukotoxin A - Pas probable RTX-famil hypothetical prote rhizobiocin/RTX to probable phosphoes	cytotoxin RTX homo iron-regulated pro iron-regulated pro iron-regulated pro hemolysin-type cal hemolysin-type cal fe-regulated RTX c bacteriocin XF2407 leukotoxin A - Pas probable RTX-famil hypothetical prote rhizobiocin/RTX to probable phosphoes hemolysin-type cal	cytotoxin RTX homo iron-regulated pro iron-regulated pro hemolysin-type cal hemolysin-type cal Fe-regulated RTX c bacteriocin XF2407 leukotoxin A - Pas probable RTX-famil hypothetical prote rhizobiocin/RTX to probable phosphoes hemolysin-type cal

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66 AKKSYDTYNQFLSLTQTGIAISATKLEKFLQKHSTNKLAKGLDSVENIDRKLGKASNVLS 125

probable secreted	в95953	2	219	5. 6	259.5	G
probable outer mem	T03516	N	1028	5.6	260	4
mannuronan C-5-ep	S77626	N	1839	5.6	261.5	w
hypothetical prot	AH2137	N	3262	5.7	262.5	2
hemolysin - Synec	S74910	N	1741	5.7	262.5	ب
probable calcium-l	E95933	N	387	5.7	263.5	40
hypothetical prote	AD1841	N	2348	5.7	266	õ
hypothetical prote	AD2263	2	589	5.7	266.5	ã
hypothetical calci	E95995	2	387	5 8	267.5	7
hypothetical prote	G95405	N	539	5.8	268	6
probable outer mer	н95964	ν	1112	5 8	269.5	ű
calcium-binding pı	G87572	2	650	5.9	276	4
hypothetical prote	AC1852	N	900	6.0	280	ũ
hypothetical prote	T03518	N	643	6.0	280	32
hypothetical prot	AG2137	N	1417	6.2	287	ñ
hypothetical prote	AH2493	2	3083	6.2	287.5	õ

# ALIGNMENTS

RESULT B30169

leukotoxin A - Pasteurella haemolytica (serotype 1)
N;Alternate names: lktA protein
C;Species: Pasteurella haemolytica
C;Date: 12-Oct-1989 #sequence\_revision 15-Nov-1996 #text\_change 18-Jun-1999
C;Accession: B30169; C32051; S29516
R;Highlander, S.K.; Chidambaram, M.; Engler, M.J.; Weinstock, G.M.
DNA 8, 15-28, 1989
A;Title: DNA sequence of the Pasteurella haemolytica leukotoxin gene cluster.
A;Reference number: A30169; MUID:89210283

A; Accession: B30169

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		NIAT 86	28 QSLTQAG-SSLKTGAKKIILYIPQNYQYDTEQGNGLQDLVKAAEELGIEVQREERNNIAT 86	KAAEELG	HODLVE	DTEQGNO	IPONYOY	AKKIILY	-SSLKTG	SLTOAG	28 (	ДĎ		al	cal
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rep	tandem	orotein;	C; Keywords: calcium binding; cytolysis; exotoxin; hemolysis; lipoprotein; tandem rep	hemolys	xin; }	; exoto	tolysis	ling; cy	um bind	: calci	eywords	C;K		homo	р
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								A; Description: lyses leukocytes	ses leu	ion: ly:	escript	A;D		ö	ase
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•	fever)	shipping	C;Comment: This organism causes bovine pneumonic pasteurellosis (shipping fever).	asteure	onic pa	pneumo	bovine	causes	rganism	This o	omment:	0;0		Ç.	Act
	•	D: g150494	A;Cross-references: EMBL:M20730; NID:g150492; PIDN:AAA25529.1; PID:g150494	: AAA255	PIDN	150492;	; NID:9	::M20730	S: EMBL	ference	ross-re	A;C		Esch	ES
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									16	n: S295	A; Accession: S29516	A; A		tino	Ë
						837	A; Reference number: S29515; MUID: 87306837	15; MUI	r: S295	e numbe:	eference	A; R		οb	inob
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							987	Infect. Immun. 55, 1987-1996, 1987	, 1987-	nun. 55	ect. Im	Inf		ğ	inob
						P.E.	R;Lo, R.Y.C.; Strathdee, C.A.; Shewen, P.E	C.A.;	athdee,	C.; Stra	), R.Y.	R;L		Pas	סי
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						172	A; Reference number: A32051; MUID:89123172	51; MUI	r: A320	e numbe:	eference	A; R			
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RESULT 2
B33389
toxin II - Actinobacillus pleuropneumoniae
N.Alternate names: cytolysin II; RTX-toxin II
C; Species: Actinobacillus pleuropneumoniae
C; Date: 09-Mar-1990 #sequence_revision 01-Nov
C; Accession: B33389; S1853; B43599
R; Chang, Y.F.; Young, R.; Struck, D.K.
DNA 8, 635-647, 1989
A; Title: Cloning and characterization of a her
A; Reference number: A33389; MUID:90126233
A; Accession: B3389
A; Molecule type: DNA
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A;Cross references: EMBL:x61111; NID:g38939; PIDN:CAA43423.1; PIR;Smits, M.A.; Briaire, J.; Jansen, R.; Smith, H.E.; Kamp, E.M.; Infect. Immun. 59, 4497-4504, 1991
A;Title: Cytolysins of Actinobacillus pleuropneumoniae serotype A;Reference number: A43599; MUID:92040145
A;Accession: B43599
                             C;Superfamily: hemolysin A; hemolysin A homology C;Superfamily: hemolysin A; hemolysin A homology C;Keywords: calcium binding; cytolysis; exotoxin; hemolysis; lipoprotein; tandem F;243-787/Domain; hemolysin A homology <HIYA>
F;719-801/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIYF]-X)
                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-27;948-956 <SM2>
A;Cross-references: GB:X61111; NID:g38939
C;Comment: This organism causes porcine pleuropneumonia
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A;Cross·references: GB:M30602; NID:g141823; PIDN:AAA87232.1;
A;Experimental source: serotype 5
R;Smits, M.A.; Briaire, J.; Jansen, R.; Smith, H.E.; Kamp, E.
submitted to the EMBL Data Library, July 1991
A;Description: Cytolysins of Actinobacillus pleuropneumoniae
A;Reference number: S18852
     F;557/Binding
                                                                                                                    A; Description: C; Superfamily:
                                                                                                                                                                            A; Gene: apxIIA; C; Function:
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A; Residues: 1-956 <SMI>
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site: palmitate (Lys) (covalent) #status
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Query Match 419 396 359 336 299 276 239 216 179 157 121 97 61 37 Local Similarity μ TIEASLTTISTALGAVSAGVSAAAVGSAVGAPIALLVAGVTGLISGILEASKQAMFESVA NKVHDRIVEWEKKH-NKNYFEQGYDSRHLADLQDNMKFLINLNKELQAERVVAITQQRWD NRLQGKILEWEKQNGGQNYFDKGYDSRYAAYLANNLKFLSELNKELEAERVIAITQQRWD TIDASVTTINTALAAISGGVGAASAGSLVGAPVALLVAGVTGLITTILEYSKQAMFEHVA TGAVAALITSSIMLAISPLAFMNAADKFNHANALDEFAKQFRKFGYDGDHLLAEYQRGVG DIISGLLSGASAGLILADKEASTEKKAAAGVEFANQIIGNVTKAVSSYILAQRVASGLSS ETITGLLSGISAGFALADKNASTGKKVAAGFELSNQVIGNVTKAISSYVLAQRVAAGLST ASIDLINEIIGNLSQSTQTIEAFSSQLAKLGSTISQAKGFSNIGNKLQNL-NFSKTNLGL KHSTNKLAKGLDSVENIDRKLGKASNVLSTLSSFLGTALAGIELDSLIKKGDAAPDALAK QGNGVQDLVKAANDLGIEVWREERSNLDIAKTSFDTTQKILGFTDRGIVLFAPQLDNLLK KGGTLNDFIKAADELGIARLAEEPNHTETAKKSVDTVNQFLSLTQTGIAISATKLEKFLQ MSKITLSSLKSSLQQGLKNGKNKLNQAGTTLKNGLTQTGHSLQNGAKKLILYIPQGYDSG MSNINV--IKSNIQAGL----- ${\tt TGPVAALIASTVALAVSPLSFLNVADKFKQADLIKSYSERFQKLGYDGDRLLADFHRETG}$ AGLELTNELVGNIASSVQTVDAFAEQISKLGSHLQNVKGLGGLSNKLQNLPDLGKASLGL KNP--KIGNTLGSASSISQNIGKANTVLGGIQSILGSVLSGVNLNELLQNKDPNQLELAK Conservative 48.2%; 188; Score 2240.5; DB 1; Pred. No. 3.4e-107; 8; Mismatches 254; ·-----NSTKSGLKNLYLAIPKDYDPQ Indels Length 53; Gaps 395 335 298 275 238 215 178 120 96 60 36 358 15;

HFTSPLLTAGTESRERLTNGKYSYINKLKFGRVKNWQVTDGEASSKLDFSKVIQRVA---NQIGDLAAISRRIDKISSGKAYVDAFEEGQHQSYDSSVQLDNKNGIINISNIN-RKIQSV NNIGELAGITKLGERIKSGKAYADAFEDGKKVEAGSNITLDAKTGIIDISNSNGKKTQAL 515

572

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A: Molecule type: DNA
A: Residues: 723-955 (LA3)
A: Residues: 723-955 (LA3)
A: Cross references: EMBL: Z22887; NID: g311824; PI
A: Cross references: EMBL: Z22887; NID: g311824; PI
A: Experimental source: serotype T10
C: Function:
A: Experimental source: serotype T10
C: Function:
A: Description: attacks cell membranes and causes
C: Superfamily: hemolysin A; hemolysin A homology
C: Keywords: calcium binding: cytolysis; exotoxin
F: 240-786/Domain: hemolysin A homology CHIVA>
F: 718-809/Region: 9-residue repeats (G-G-X-G-[DN
F: 718-726/Region: repeat
                                                                                                                                                                                                                                                                                                                                                                                                 A:Molecule type: DNA
A:Residues: 950-955 +HIS>
A:Residues: 950-955 +HIS>
A:Cross-references: GB:M24197; GB:M34943; G
R:Lainson, A.F.; Aitchison, K.D.; Donachie, submitted to the EMBL Data Library, June 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:Z26247; NID:g400424; PIDN:CAA81206.1; PID:g400425 R;Highlander, S.K.; Engler, M.J.; Weinstock, G.M.
J. Bacteriol. 172, 2343-2350, 1990
A;Title: Secretion and expression of the Pasteurella haemolytica leukotoxin A;Reference number: A35254; MUID:g0236888 ·
A;Accession: A35254
A;Status: preliminary
                                                                                                                                                                                                                             A;Cross-references: EMBL:Z22884;
A;Experimental source: serotype (
A;Accession: S34235
                                                                                                                                                                                                                                                                                                                                       A; Description: DNA sequence of the carboxy terminal end A; Reference number: S34235 A; Accession: S34237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Lainson, A.F.; Aitchison, K.; Donachie, W. submitted to the EMBL Data Library, September A;Description: DNA sequence of the leukotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N;Alternate names: lktA protein
C;Species: Pasteurella haemolytica
C;Date: 10-Aug-1990 #sequence_revision 15-Nov-1996 #text_change 18-Jun-1999
C;Accession: S37145; A35254; S34237; S34235
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A; Residues: 745-955 <LA2>
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                                           ;Keywords: calcium binding; cytolysis; exotoxin;;240-786/Domain: hemolysin A homology <HLYA>
                                                                                   Description: attacks cell membranes and causes; Superfamily: hemolysin A; hemolysin A homology
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                       (G-G-X-G-[DN]-D-X-[LVIYF]-X)
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    ---ITSNLQNYQSNKTDHKIEQLIGKDGSYITSDQIDKILQDKKDGTVITSQELKKLADE
                                             DIFVHRQGDGNDSITESEGNDKLSFSDSNLKDLTFEKVNHHLVI-TNTKQEKVTIQNWFR
                                                                                   DVYIFRKGDGNDTLYDGTGNDKLAFADANISDIMIERTKEGIIVKRNDHSGSINIPRWY-
                                                                                                                                                  KGSKFNDIFHSGEGDDLLDGGAGDDRLFGGKGNDRLSGDEGDDLLDGGSGDDVLNGGAGN
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                                                                                                                              KGSKFNDAFNGGDGVDTIDGNDGNDRLFGGKGDDIIDGGNGDDFIDGGKGNDLLHGGKGD
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458; Conserv
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Pred. No. 5.9e-107;
8; Mismatches 271;
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725

785

607

580 547 487

666

407

367 347

427

307 287 247 227 187 168 128 71 48

17;

876

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A;Accession: A43834
A;Kolecule type: DNA
A;Rolecule type: DNA
A;Residues: 1-956 CBUR>
A;Experimental source: isolate 3714
A;Note: sequence extracted from NCBI backbone (NCBIN:104212, NCBIP:104211)
C;Comment: This organism causes acute fatal septicemia in young pigs.
C;Function: attacks cell membranes and causes cell lysis
C;Function: attacks cell membranes and causes cell lysis
C;Superfamily: hemolysin A; hemolysin A homology
C;Keywords: calcium binding; cytolysis; exotoxin; hemolysis; lipoprotein;
F;243-787/Domain: hemolysin A homology <HIXA>
F;719-801/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIYF]-X)
F;557/Binding site: palmitate (Lys) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
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Infect. Immun. 60, 2166-2173, 1992
, Title: Molecular characterization of an A; Reference number: A43834; MUID:92267623
A; Accession: A43834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; Burrows, L.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       toxin II - Actinobacillus suis
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Best Local Similarity
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                                                                                                  NRLQGKILEWEKQNGGQNYFDKGYDSRYAAYLANNLKFLSELNKELEAERVIAITQQRWD 455
                                                                                                                                                                                                                                                                                                                                DIISGLLSGASAGLILADKKASTEKKAAAGVEFANQIIGNVTKAVSSYILAQRVASCLSS
                                                                                                                                                                                                                                                                                                                                                                                                                                     ASIDLINEIIGNLSQSTQTIEAFSSQLAKLGSTISQAKGFSNIGNKLQNL-NFSKTNLGL 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KGGTLNDFIKAADELGIARLAEEPNHTETAKKSVDTVNQFLSLTQTGIAISATKLEKFLQ 96
NQIGDLAAISRRTDKISSGKAYVDAFEEGQHQSYDSSVQLDNKNGIINISNTN-RKTQSV
                                                                             NKVHDRIVEWEKKH-NKNYFEQGYDSRHLADLQDNMKFLINLNKELQAERVVAITQQRWD
                                                                                                                                                                                                                                              {\tt TGPVAALIASTVALAVSPLSFLNVADKFKQADLIKSYSERFQKLGYDGDRLLADFHRETG}
                                                                                                                                                                                                                                                                    TGAVAALITSSIMLAISPLAFMNAADKFNHANALDEFAKQFRKFGYDGDHLLAEYQRGVG
                                                                                                                                                                                                                                                                                                                                                                       EIITGLLSGISAGFALADKNASTGKKVAAGFELSNQVIGNVTKAISSYVLAQRVAAGLST 275
                                                                                                                                                                                                                                                                                                                                                                                                                {\tt AGLELTNELVGNIASSVQTVDAFAEQISKLGSHLQNVKGLGGLSNKLQNLPDLGKASLGL}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KNP:-KIGNTLGSASSISQNIGKANTVLGGIQSILGSVLSGVNLNELLQNKDPNQLELAK 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KHSTNKLAKGLDSVENIDRKLGKASNVLSTLSSFLGTALAGIELDSLIKKGDAAPDALAK 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QGNGVQDLVKAANDLGIEVWREERSNLDIAKTSFDTTQKILGFTDRGIVLFAPQLKNLLK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EAEFAKTIQNYVATR-DDKIEEIIGQNGERITSKQVDELIE--KGNGKIAQSELTKVVDN 901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NKSQKLSASDIASSLNKLVGSMALFGTANSVSSNALQPITQPTQGILAPSV 927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     451;
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Pred. No. 1.3e-105;
37; Mismatches 259;
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A;Description: lyses lung macrophages (S;Superfamily: hemolysin A; hemolysin A homology (S;Superfamily: hemolysin A; hemolysin; homology (S;Eqwords: calcium binding; cytolysis; exotoxin; lipoprotein; tandem F;254-804/Domain: hemolysin A homology (HIYA) (F;736-862/Region: 9-residue repeats (G-X-G-[DN]-D-X-[LVIYF]-X) F;736-862/Region: 9-residue repeats (G-X-G-[DN]-B-X-[LVIYF]-X) F;571,702/Binding site: palmitate (Lys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Jansen, R.; Briaire, J.; van Geel, A.B.M.; Kamp, Infect. Immun. 62, 4411-4418, 1994
A;Title: Genetic map of the Actinobacillus pleuropi A;Reference number: S48042; MUID:95012630
A;Accession: S48043
                                                                                                                                                                                                                                                       A; Experimental source: strain 405, serotype 8
A; Note: the nucleotide sequence was submitted to the EMBL Data C; Comment: This orgnism causes porcine pleuropneumonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:X68815; NID:g38956; PIDN:CAA48711.1; PID:g38958 A;Experimental source: strain 405, serotype A;A;Note: sequence extracted from NCBI backbone (NCBIN:125168, NCBIP:12517 A;Note: sequence extracted from NCBI backbone (NCBIN:125168, NCBIP:12517 R;Jansen, R.; Briaire, J.; yan Geel, A.B.M.; Kamp, E.M.; Gielkens, A.L.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      toxin III - Actinobacillus pleuropneumoniae N;Alternate names: RTX-toxin III (ApxIIIA) C;Species: Actinobacillus pleuropneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
B49219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Title: Cloning and characterization of the A; Reference number: A49219; MUID:93162836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Date: 19-Dec-1993 #sequence_revision 01-Nov-1996
C;Accession: B49219; S48043; S29958
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                                                                                                                                                                               C; Function:
                                                                                                                                                                                                        A; Gene:
                                                                                                                                                                                                                                   C; Genetics:
                                                                                                                                                                                                                                                                                                                                        A; Cross-references: EMBL: X80055; NID: g558150;
                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-1052 < JAN2>
                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary; nucleic acid sequence not shown;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-1052 < JAN1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: B49219
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Infect. Immun. 61, 947-954, 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NQISAEALSKVVNDYNTSK-DRQNVSNSLAKLISSVGSFTSSSDFRNN
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                                                                                                                             HNNGVLTIKDWF-----KEGNKYNHKIEQIVDKNGRKLTAENLGTYFKNAPKADNLLN
                                                                                                                                                       ---GSINIPRWYITSNLQNYQSNKTDHKIEQLIGKDGSYITSDQIDKILQDKKDGTVITS
                                                                                                                                                                                                                 LNGGAGNDVYIFRKGDGNDTLYD---GTGNDKLAFADANISDIMIERTKEGIIVKRNDHS
                                                                                                                                                                                                                                              EGNDKLLGGNGNNYLSGGDGNDELQVLGNGFNVLRGGKGDDKLYGSSGSDLLDGGEGNDY
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C:Function:

A:Description: lyses lung macrophages
A:Description: lyses lung macrophages
C:Superfamily: hemolysin A; hemolysin A homology
C:Superfamily: hemolysin A; hemolysis; exotoxin; lipoprotein; tandem repeat; thioles
C:Keywords: calcium binding; cytolysis; exotoxin; lipoprotein; tandem repeat; thioles
F:254-803/Domain: hemolysin A homology <HLYA>
F:35-861/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIYF]-X)
F:571,702/Binding site: palmitate (Lys) (covalent) #status predicted
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C;Species: Actinobacillus pleuropneumoniae
C;Date: 14-Jul-1995 #sequence_revision 15-Nov-1996
C;Accession: S51784
R;Chang, Y.F.; Shi, J.; Ma, D.P.; Shin, S.J.; Lein,
DNA Cell Biol. 12, 351-362, 1993
A;Title: Molecular analysis of the Actinobacillus p
A;Reference number: S51783; MUID:93263992
A;Accession: S51784
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A; Gene: apxIIIA
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                                  VAETEGTDEIGLIVNAKAGNDDIFVGQGKMNIDGGDGHDRVFYSKDGGFGNITVDGTSAT 630
                                                                                                                                                                            GITKLGERIKSGKAYADAFEDGKKVEAG----SNITLDAKTGIIDISNSNGKKTQALHFT 518
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                                                                                                    SPLLTAGTESRERLTNGKYSYINKLKFGRVKNWQVTDG--EASSKLDFSKVIQR-----
                                                                                                                                                        GITGKGDKLSSGKAYVDYFQEGKLLEKKPDDFSKVVFDPTKGEIDISNS--QTSTLLKFV
                                                                                                                                                                                                                                      DEWEKKY-GKNYFENGYDARHKAFLEDSFSLLSSFNKQYETERAVLITQQRWDEYIGELA
                                                                                                                                                                                                                                                                         LEWEKQNGGQNYFDKGYDSRYAAYLANNLKFLSELNKELEAERVIAITQQRWDNNIGELA 462
                                                                                                                                                                                                                                                                                                                    TISTALSAIAAGTAAASAGALVGAPITLLVTGITGLISGILEFSKQPMLDHVASKIGNKI 436
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43.1%;
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Pred. No. 4.1e-91;
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C;Superfamily: hemolysin A; hemolysin A homology
C;Keywords: lipoprotein
F;247-792/Domain: hemolysin A homology <HLYA>
F;564,690/Binding site: palmitate (Lys) (covalen)
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A; Residues: 1-1024 <HES>
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A;Reference number: S07209
A;Accession: S10056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: S10056 R;Hess, J.; Wels, W.; Vogel, M.; Goebel, W. FEMS Microbiol. Lett. 34, 1-11, 1986
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C;Date: 19-Mar-1997
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C;Species: Escherichia coli
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                                              VSGILSAISASFILSNADADTRTKAAAAGVELTTKVLGNVGKGISQYIIAQRAAQGLSTSA
                                                               IELINQLVDTVASLNNNVNSFSQQLNTLGSVLSNTKHLNGVGNKLQNLPNLDNIGAGLDT
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41.5%;
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Pred. No. 3.4e-87;
3; Mismatches 308
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A;Cross references: GB:M10133; GB:M12863; NID:g146377; PIDN:AAA23975.1; A;Experimental source: strain J96, O4 serotype R;Stanley, P; Packman, L.C.; Koronakis, V.; Hughes, C. Science 266, 1992-1996, 1994
A;Title: Fatty acylation of two internal lysine residues required for the A;Reference number: A55387; MUID:95099325
A;Contents: annotation; lysine palmitoylation A;Note: lysine modification is performed by the hlyC gene product
                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-1023 <FEL>
                                                                                                                                                                    A; Reference number: A; Accession: A24433
                                                                                                                                                                                A; Title: Nucleotide sequence of an Escherichia A; Reference number: A24433; MUID:85234404
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;Date: 30-Sep-1988 #sequence_revision 30-Sep-1988
;Accession: A24433; I41280
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601 572 541 513 483 457 424

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953 860 898 808

PID:g146379

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R; Haertlein, M.; Schiessl, S.; Wagner, W.;
J. Cell Biol. 22, 87-97, 1983
A; Title: Transport of hemolysin by Escheric
A; Reference number: I41280
A; Reference number: I41280
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1, 'T', 3, 'V', 5, 'T', 7-44 <RES>
A; Molecule type: DNA
A; Residues: 1, 'T', 3, 'V', 5, 'T', 7-44 <RES>
A; Cross-references: GB:MZ9173; NID:g146337;
A; Gene: hlyA
C; Genettcs:
A; Gene: hlyA
C; Function: attacks blood cell membranes
C; Superfamily: hemolysin A; hemolysin A hom
C; Keywords: calcium binding; cytolysis; ex
F; 246-791/Domain: hemolysin A; homology <HLY
F; 723-81/Region: 9-residue repeats (G-G-X
F; 563,689/Binding site: palmitate (Lys) (cc
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  889
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  VEEVIGSQFNDVFKGSKFNDIFHSGEGDDLLDGGAGDDRLF-
                                                                             EAGSYTVNRKVARGD--IYHEVVKRQETKVGKRTETIQYRDYELRKV-GYGYQSTDNLKS
                                                                                                                       VGNNQYREIRIESHLGDGDDKVFLSAGSANIYAGKGHDVVYYDKTDTGY--LTIDGTKAT
                                                                                                                                             ETEGT-DEIGLIVNAKAGNDDIFVGQGKMNIDGGDGHDRVFYSK-DGGFGNITVDGTSAT
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                                          EAGNYTVTR-VLGGDVKVLQEVVKEQEVSVGKRTEKTQYRSYEFTHINGKNLTETDNLYS
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54; Mismatches
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4.5e-87;
hes 306;
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C;Species: Actinobacillus actinomycetemcomitans
C;Date: 16-Sep-1992 #sequence\_revision 01-Nov-1996 #text\_change 31-Mar-2000
C;Accession: A37205; A60768; B34345; A32276; PH0267; PH0266; S17284 R; Kraig, E.; Dailey, T.; Kolodrubetz, Infect. Immun. 58, 920-929, 1990 C; Accession: A; Molecule type: DNA A; Residues: 1-1055 < A; Title: Nucleotide sequence of the leukotoxin A; Reference number: A37205; MUID:90202154 A;Accession: A37205 leukotoxin A - Actinobacillus actinomycetemcomitans <KRA> D. gene from sequence is correct Actinobacillus actinomyceten

R; Kolodrubetz, D.; Dailey, T.; Ebersole, Infect. Immun. 57, 1465-1469, 1989 sing nucleotide A;Cross-references: GB:X16829; NID:g38643; PIDN:CAA34731.1; PID:g38645 A;Note: the authors present evidence that the nucleotide sequence is co J.; Kraig, E. from Actinobacillus 'n the

A;Title: Cloning and expression of the leukotoxin gene A;Reference number: A60768; MUID:89212893 A;Accession: A60768

A; Molecule type: DNA A; Residues: 297-309,'Y',311-364;434-440,'KC',443-474,'H',476-489,'S',491-493,'YLK',49 A; Status: nucleic acid sequence not shown; not compared with conceptual translation

A;Note: this sequence is revised in reference A37205
R;Lally, E.T.; Golub, E.E.; Kieba, I.R.; Talchman, N.S.; Rosenbloom, J.;
Biol. Chem. 264, 15451-15456, 199
A;Title: Annalysis of the Actinobacillus actinomycetemcomitans leukotoxin A;Reference number: A34345; MUID:89359382
A;Accession: B34345

gene. Rosenbloom,

Deline

A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-239, 'Y', 241-259, 'H', 261-335, 'A', 337-415, 'S', 417-438, 'S', 440-723, 'N', 72!
A;Residues: GL-239, 'Y', 241-259, 'H', 261-335, 'A', 337-415, 'S', 417-438, 'S', 440-723, 'N', 72!
PVKRYPLRHCRPITLTLTQIR' <LAL>
A;Cross references: GB.M27933
R;Lally, E.T.; Kieba, I.R.; Demuth, D.R.; Rosenbloom, J.; Golub, E.E.; Taichman, N.S.
Blochem. Blophys. Res. Commun. 159, 256-262, 1989
A;Title: Identification and expression of the Actinobacillus actinomycetemcomitans 14
A;Reference number: A32276; MUID:89165863
A;Accession: A32276

A;Status: nucleic acid sequence not shown; not compared with conceptual translation

A; Note: this sequence is revised in refer R; Ohta, H.; Miyagi, A.; Kato, K.; Fukui, submitted to JIPID, July 1995 A; Description: Modulation of leukotoxin | A;Molecule type: DNA
A;Residues: 430-438,'S',440-476,'R',478-506,'RVRS',511,'QSIAINSLNTD',523-541,'I',543.
A;Note: this sequence is revised in reference A34345
DONATA H: Mivagi, A.; Kato, K.; Fukui, K.

A; Reference number: PH0266 A; Accession: PH0267 leukotoxin production γģ growth rate and bicarbonate 'n

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A; Molecule type: protein
A; Residues: 2-6, 'L', 8-26 <
C; Genetics:
A; Gene: ltxA
C; Function:
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A; Experimental source: strain
A; Accession: PH0266
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nes 298;
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A:Description: attacks blood cell membranes and causes cell lysi C;Superfamily: hemolysin A; hemolysin A homology C;Keywords: calcium binding; cytolysis; extoxin; hemolysis; lip:E;243-789/Domain: hemolysin A homology cHIYA>
E;721-847/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LYIYF]-X) F;560,686/Binding site: palmitate (Lys) (covalent) #status predi
                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-209,'AMPYLTLA',218-373,'R',375-561,'Q',563-686,'TC',688-1022 <RE2>
A;Cross-references: EMBL:X68595; NID:g505568; PIDN:CAA48586.1; PID:g505570
R:Tascon, R.I.; Vazquez-Boland, J.A.; Gutierrez-Martin, C.B.; Rodriguez-Barbosa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Actinobacillus pleuropneumoniae
C;Date: 19-Unl-1996 #sequence_revision 08-Nov-1996 #text_change 18-Jun-1999
C;Accession: 139643; S18769; T39645; S60732; S35781
R,Jansen, R.; Briaire, J.; Kamp, E.M.; Glelkens, A.L.; Smits, M.A.
Infect. Immun. 61, 3688-3695, 1993
A;Title: Structural analysis of the Actinobacillus pleuropneumoniae-kTX-toxin
A;Reference number: 139641; MUID:93366425
                                                                                                                                                        C; Function:
                                                                                                                                                                                  A;Gene: apxIA
                                                                                                                                                                                                         C; Genetics:
                                                                                                                                                                                                                                    C; Comment: This
                                                                                                                                                                                                                                                                                A; Molecule type:
                                                                                                                                                                                                                                                                                                                                  A; Title: The RTX haemolysins ApxI and ApxII are major virulence A; Reference number: S60731; MUID:95131743
A; Accession: S60732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Title: Sequence analysis and transcription of the A; Reference number: I39644; MUID:94237497 A; Accession: I39645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Restidues: 1-209, 'ANPYLTLA', 218-373,'R', 375-561,'Q', 563-686,'TC', 688-1022
A; Cross-references: EMBL: X52899; NID: g38949; PIDN: CAA37081.1; PID: g38950
R; Frey, J.; Haldimann, A.; Nicolet, J.; Boffini, A.; Prentki, P.
Gene 142, 97-102, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Nucleotide sequence of the hemolysin A;Reference number: S18769; MUID:91348845 A;Accession: S18769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross references: EMBL:X73117; NID:g312897; A;Frey, J.; Meier, R.; Gygi, D.; Nicolet, J. Infect. Immun. 59, 3026-3032, 1991
                                                                                                                                                                                                                                                              A; Residues:
                                                                                                                                                                                                                                                                                                     A; Status: preliminary; not
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A; Residues: 1-1022 < RES>
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N;Alternate names: hemolysin ApxI
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                                                                                                                                                                                                                              VLKEVVKTQDISVGKRSEKLEYRDYELSPFELGNGIRAKDELHSVEEIIGSNRKDKFFGS
                                                                                                                                                                                                                                                                                 IYHEVVKRQETKVGKRTETIQYRDYELR--KVGYGYQSTDNLKSVEEVIGSQFNDVFKGS
                                                                                                                                                                                                                                                                                                                   EKNDRIYLSSGSSIVYAGNGHDVAYYDKTDTGY--LTFDGQSAQKAGEYIVTKELKADVK
                                                                                                                                                                                                                                                                                                                                               -- NDDIFVGQGKMNIDGGDGHDRVFYSK-DGGFGNITVDGTSATEAGSYTVNRKV-ARGD
                                                                                                                                                                                                                                                                                                                                                                                                 RLTNGKYSYINKLKFGRVKNWQVTDGEASSKL-DFSKVIQRVAETEGTDEIGLIVNAKAG
                                                                                                                                                                                                                                                                                                                                                                                                                            KAYADAFEDGKKVEAG----SNITLDAKTGIIDISNSNGKKTQALHFTSPLLTAGTESRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SFLNVADKFERAKQLEQYSERFKKFGYEGDSLLASFYRETGAIEAALTTINSVLSAASAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TQTALSALQSFLGTAIAGMDLDSLLRRRRNGEDVSGSELAKAGVDLAAQLVDNIASATGT
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YN---ALPQLRKDIEQIISSTGAFTGDHGKVSVGSGGPL
                       KSQKLSASDIASSLNKLVGSMALF-GTANSVSSNALQPI 915
                                                                           WYITSNLONYOSNKTDHKIEQLIGKDGSYITSDQIDKILQDKKDGTVITSQELKKLADEN
                                                                                                     YGRHIIIEKGGDDDTLLLSDLSFKDVGFIRIGDDLLVNKRIGGTLYYHEDYNGNALTIKD
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                                                                                                                                                          NGGDGDDELQVFEGQYNVLLGGAGNDILYGSDGTNLFDGGVGNDKIYGGLGKDIYRYSKE
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C;Species: Escherichia coli plasmid C;Species: Escherichia coli C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #t C;Accession: T00227; T42148 R;Makino. K · Talif
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C;Superfamily: hemolysin A; hemolysin A homology
C;Keywords: cytolysis; hemolysis; lipoprotein; toxin
F;233-776/Domain: hemolysin A homology <HLYA>
F;550,675/Binding site: palmitate (Lys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:AB011549; NID:g4589740; PIDN:BAA31774.1; PID:g3337015 A;Experimental source: strain EHEC O157:H7, substrain RIMD 0509952 R;Bulland, V.; Shao, Y.; Perna, N.T.; Plunkett, G.; Sofia, H.J.; Blattner, F.R Nucleic Acids Res. 26, 4196-4204, 1998 A;Title: The complete DNA sequence and analysis of the large virulence plasmid A;Reference number: Z22068; MUID:98391744 A;Accession: T42148
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A; Residues: 1-998 <BUR>
A; Cross-references: EMB
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DNA Res. 5, 1-9, 1
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                                                                                                                                             KFNHANALDEFAKQFRKFGYDGDHLLAEYQRGVGTIEASLTTISTALGAVSAGVSAAAVG 361
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KFERAKQLESYSERFKKLNYEGDALLAAFHKETGAIDAALTTINTVLSSVSAGVSAASSA 374
                                                                                                                                                                                                                                           VAAGFELSNQVIGNVTKAISSYVLAQRVAAGLSTTGAVAALITSSIMLAISPLAFMNAAD
                   RYAAYLANNLKFLSELNKELEAERVIAITQQRWDNNIGELAGITKLGERIKSGKAYADAF
                                                                        SAVGAPIALLVAGYTGLISGILEASKQAMFESVANRLOGKILEWEKQNGGQNYFDKGYDS 421
                                                                                                                                                                                                                          AAAGIELTTQVLGNVGKAVSQYILAQRMAQGLSTTAASAGLITSAVMLAISPLSFLAAAD
                                                                                                                                                                                                                                                                                                  LNQLGSFLSSKPRLSSVGGKLQNLPDLGPLGDGLDVVSGILSAVSASFILGNSDAHTGTK
                                                                                                                                                                                                                                                                                                                        LAKLGSTISQAKGFSNIGNKLQNL-NFSKTNLGLEIITGLLSGISAGFALADKNASTGKK 241
                                                                                                                                                                                                                                                                                                                                                                           LQNFTGIALSGMALDELLRKQREGEDISQNDIAKSSIELINQLVDTVSSINSTVDSFSEQ
                                                                                                                                                                                                                                                                                                                                                                                             LSSFLGTALAGIELDSLIKK----GDAAPDALAKASIDLINEIIGNLSQSTQTIEAFSSQ 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                    KSVDTVNQFLSLTQTGIAISATKLEKFLQKHSTNKLAKGL-DSVENIDRKLGKASNVLST 126
RHAAFLEDSLSLLADFSRQHAVERAVAITQQHWDEKIGELAGITRNADRSQSGKAYINYL
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be: strain EDL933; serotype O157:H7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37.7%; Score 1752; DB 2;
40.1%; Pred. No. 4.1e-82;
tive 177; Mismatches 307
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Infect. Immun. 63, 1055-1061, 1995

N.Title: Molecular analysis of the plasmid-encoded hemolysin of Reference number: 141077; MUID:95172699

A.Accession: 141078

A.Status: preliminary; translated from GB/EMBL/DDBJ

A.Molecule type: DNA

A.Residues: 1-998 <RESS

A.Gross-references: EMBL:X79839; NID:g860924; PIDN:CAA56234.1; PC:Superfamily: hemolysin A; hemolysin A homology

C:Superfamily: hemolysin A; hemolysin A homology

F:233-776/Domain: hemolysin A homology <HLYA>

F:550,675/Binding site: palmitate (Lys) (covalent) #status predi
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C;Species: Escherichia coli
C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 21-Jul-2000
C;Accession: I41078
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Infect. Immun. 63, 1055-1061, 1995
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     LONFTGIALSGMALDELLRKOREGEDISONDIAKSSIELINOLVDTVSSINSTVDSFSEO
                                   LSSFLGTALAGIELDSLIKK----GDAAPDALAKASIDLINEIIGNLSQSTQTIEAFSSQ
                                                                   QFFGAAEKVVGLTERGVAIFAPQLDKLLQKY--QKVGSKIGGTAENVGNNLGKAGTVLSA
                                                                                       KSNIQAGLNSTKSGLKNLYLAIPKDYDPQKGGTLNDFIKAADELGIARLAEEPNHTETAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGSSEVFAGEGYDTVSYNKT-DVGKLTIDATGASKPGEYIVSKNM-YGDVKVLQEVVKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KGDRLHLSDISFDDIAFKRVGNDLIMNKAINGVLSFNESNDVNG-ITFKNWFAKD-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYINKLKFGRVKNWQVTDGEASSK--LDFSKVIQRVAETEGTDEIGLIVNAKAGNDDIFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EDGKKVEAG----SNITLDAKTGIIDISNSNGKKTQALHFTSPLLTAGTESRERLTNGKY
                                                                                                                                                                                                      Similarity 39.9
90; Conservative
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39.9%;
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                                                                                                                                                                                                      174;
                                                                                                                                                                                                  Score 1733; DB 2;
Pred. No. 3.8e-81;
74; Mismatches 312
                                                                                                                                                                                                                                                                                                                                              PIDN:CAA56234.1;
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                                                                                                                       adenylate cyclase hemolysin - Bordetella bronchiseptica c;Species: Bordetella bronchiseptica C;Decies: Bordetella bronchiseptica C;Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change C;Accession: S51672
R;Betsou, F; Sismeiro, O.; Danchin, A.; Guiso, N.
A; Molecule type: DNA
A; Residues: 1-1705 <BET>
A; Cross-references: EMBL: Z37112
                                                                        submitted to the EMBL Data Library, September 1994 A; Description: The adenylate cyclase-hemolysin gene A; Reference number: $51672
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S51672
                                                               A; Reference number: A; Accession: S51672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EDGKKVEAG----SNITLDAKTGIIDISNSNGKKTQALHFTSPLLTAGTESRERLTNGKY
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712

788 742 668

610 595 551 537 493

653

481 433 421 374

314 301 254 241

Bordetella

bronchiseptica

16-Jul-1999

887 955

902 827 848 778

calmodulin-sensitive adenylate cyclase catalytic domain homo:

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C;Superfamily: cyclolysin, carrell.
C;Keywords: tandem repeat
F;15-328/Domain: calmodulin-sensitive adenylate cyclase catalytic domain homology
F;543-1084/Domain: hemolysin A homology <HLYA>
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Best Local Similarity 27.8
Matches 255; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VFVDRFIQGERV-AGQPVVLDVAAGGIDIASRKGER-PALTFITPLAAPGEEQRRRTKTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAASVVGAPVAVVTSLLTGALNGILRGVQQPIIEKLANDYARKI---DELGGPQAYFEKN 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LVQQSHYADQLDKLAQESSAYGYEGDALLAQLYRDKTAAEGAVAGVSAVLSTVGAAVSIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----DALAKASIDLINEIIGNLSQ-----STQT-IEAFSSQLAKLG------STI 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLDSVENIDRKLGKASNVLSTLSSFLGTALAGIELDSLI----KKGDAAP-----
                                                                                                                                                                                                                                                                                                                                  EGDDLLDGGAGDDRLFGGKGNDRLSGDEGDDL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LQARH-EQLANSDGLRKMLADLQAGWNASSVIGVQTTEISKSALELAAITGNADNLKSAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YDSRYAAYLANN---LKFLSELNKELEAERVIAITQQRWDNNIGELAGITKLGERIKSGK 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AVGSAVGAPIALLVAGVTGLISGILEASKQAMFESVANRLQGKILEWEKQNGGQNYFDKG 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AADKFNHANALDEFAKQFRKFGYDGDHLLAEYQRGVGTIEASLTTISTALGAVSAGVSAA 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGFELSNQVIGNVTKAISSYVL----AQRVAAGLSTTGAVAALITSSIMLAISPLAFMN 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GQRALQGAQAVAAAQRLVHAIALMTQFGRAGSTNTPQEAASLSAAVFGLGEASSAVAETV
                                                                                                                                                       WGHDGNDTIHGRRGDDILRGGLGLDTLYGEDGNDIFLQDDETVSDDIDGGAGLDTVDYAA 1213
                                                                                                                                                                                                                                                                                                              AGDDRLDGGAGNDTLVGGEGHNTVVGGAGDDVFLQDLGVWSNQLDGGAGVDTVKYNVHQP 109:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VLANASRIHYDGGAGTNTVSYAALGRQDSITV----SADGERFNVRKQLNNANVYREGVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IFVGQGKMNIDGGDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNRKVARGDIYHEVVK 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KSEFTTFVETVGKQDRWRTRDGAADTTIDLAKVVSQLVDANGVLKHSIKLEVIGGDGDDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGFFRGSSRWAGGFGVAG------GAMALGGGIGAVGAGMSLTD-DAPAGQKA 564
                                                                           MI----HAGNIVAPHEYGFGIEADLSEGWVRKAARRGMDYYDSVRSVENVIGTSMKD-VL 1268
                                                                                                                                                                                           NGGAGNDVYIFRKGD-----GNDTLYDGTGNDKLAFADANISDIM-----IERTKEGI 802
                                                                                                                                                                                                                                    SEERLERMGDTGIHADLQKGTVEKWPALNLFSVDHVKNIENLHGSSLNDSIAGDDRDNEL 1153
                                                                                                                                                                                                                                                                                                                                                                                           TQKTAYGKRTENVQYRHVELARVGQ-LVEVDTLEHVQHIIGGAGNDSITGNAHDNFLAGG
IGDAQANTLMGQGGDDTV 1286
                                  ITSDQIDKILQDKKDGTV
                                                                                                                IVKRNDHSGSINIPRWY - - - ITSNLQNYQSNKTDHK - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----QAKGFSNIGNKLQNLNFSKTNLGLEIITGLLSGISAGFALADKNASTGKKV 242
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27.8%;
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A;Title: Secretion of cyclolysin, the calmodulin-sensitive adenylate cyclase-haemol. A;Reference number: S02386; MUID:89091151
A;Contents: annotation; identification of adenylate cyclase-hemolysin bifunctional | R;Munier, H; Gilles, A,M; Glaser, P; Krin, E; Danchin, A.; Sarfati, R.; Barzu, O Eur. J. Biochem. 196, 469-474, 1991
A;Title: Isolation and characterization of catalytic and calmodulin-binding domains A;Reference number: S14100; MUID:91177021
A;Accession: S14100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: cyclolysin; calmodulin-sensitive adenylate cyclase catalytic domain he;Keywords: calcium binding; calmodulin binding; cAMP biosynthesis; carbon-oxygen ly;F;15-328/Domain: calmodulin-sensitive adenylate cyclase catalytic domain homology cALF;25-35/Region: calmodulin binding #status predicted F;25-65/Region: calmodulin binding #status predicted F;59-66/Region: nucleotide binding #status predicted F;54-1085/Domain: hemolysin A homology cHLVA>
F;1033-1041,1042-1050,1174-1182,1289-1297,1298-1308,1316-1324,1430-1438,1556-1564/Rei
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A; Molecule type: protein
A; Residues: 1-78, 'M', 80, 'M', 82-97, 'M', 99-139, 'M', 141-178, 'M', 180-399
A; Residues: 1.78, 'M', 80, 'M', 82-97, 'M', 99-139, 'M', 141-178, 'M', 180-399
A; Residues: 1.78, 'M', 80, 'M', 82-97, 'M', 99-139, 'M', 141-178, 'M', 180-399
A; Residues: 1.78, 'M', 80, 'M', 82-97, 'M', 99-139, 'M', 141-178, 'M', 180-399
A; Residues: 1.78, 'M', 80, 'M', 82-97, 'M', 99-139, 'M', 141-178, 'M', 180-399
A; Residues: 1.78, 'M', 80, 'M', 82-97, 'M', 99-139, 'M', 141-178, 'M', 180-399
A; Residues: 1.78, 'M', 80, 'M', 82-97, 'M', 99-139, 'M', 141-178, 'M', 180-399
A; Residues: 1.78, 'M', 80, 'M', 82-97, 'M', 99-139, 'M', 141-178, 'M', 180-399
A; Residues: 1.78, 'M', 80, 'M', 82-97, 'M', 99-139, 'M', 141-178, 'M', 180-399
A; Residues: 1.78, 'M', 80, 'M',
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C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Jul-1999
C;Accession: S00893; S14100; S02389
R;Glaser, P.; Ladant, D.; Sezer, O.; Pichot, F.; Ullmann, A.; Danchin, A.
Mol. Microbiol. 2, 19-30, 1988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Hackett, M.; Guo, L.; Shabanowitz, J.; Hunt, D.F.; Science 266, 433-435, 1994
A;Title: Internal lysine palmitoylation in adenylate A;Reference number: A55167; MUID:95025937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Title: The calmodulin-sensitive adenylate cyclase of A; Reference number: S00893; MUID:88216178
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N;Alternate names: adenylate cyclase precursor; calmodulin-sensitive adenylate cycla:
N;Contains: adenylate cyclase (EC 4.6.1.1), calmodulin-sensitive; hemolysin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;983/Binding site: palmitate (Lys) (covalent) #status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-1706 <GLA>
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Best Local Similarity
Matches 247; Conserv
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     637
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                                                                                                                                                                                                                                                                                           GNVTKAISSYVL----AQRVAAGLSTTGAVAALITSSIMLAISPLAFMNAADKFNHANAL
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     DKLAQESSAYGYEGDALLAQLYRDKTAAEGAVAGVSAVLSTVGAAVSIAAAASVVGAPVA
                                                                                                DEFAKQFRKFGYDGDHLLAEYQRGVGTIEASLTTISTALGAVSAGVSAAAVGSAVGAPIA 369
                                                                                                                                                                                                GGTVELASSIALALAAARGVTSGLQVAGASAGAAAGALAAALSPMEIYGLVQQSHYADQL
                                                                                                                                                                                                                                                                                                                                                                                                           SGFFR-GSSRWAGGFGVAGGAMALGGGIAAAVGAGMSLTD-DAPAGQKAAAGAEIALQLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KGFSNIGNKLQNLNFSKTNLGLEIITGLLSGISAGFALADKNASTGKKVAAGFELSNQVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------DALAKA-----SIDLINEI----IGNLSQSTQTIEAFSSQLAKLGSTISQ-A 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      346;
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RESULT 15
S35027
Cytotoxin RTX homolog frpC - Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 08-Oct-1999
C;Accession: S35027
R;Thompson, S.A.; Wang, L.L.; Sparling, P.F.
MO1. Microbiol. 9, 85-96, 1993
A;Title: Cloning and nucleotide sequence of frpC, a second gene from Neisseria meningiti
A;Accession: S35026; MUID:94018616
A;Accession: S35027
B,Moloculus (1993)
A;Accession: S35026; MUID:94018616
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Best Local Similarity
Watches 237; Conserva
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A;Residues: 1-1829 <THO>
A;Cross-references: GB:L06299; NID:g293961; PIDN:AAA99902.1; PID:g293963
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                                            478 DNTKLADGSFAKHGYAALAELDSNGDNIINAADAAFQTLRVWQDLNQDGIS----- 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     812 SINIPRWY---ITSNLQNYQSNKTD------HKIEQLIG---KDGSYITSDQIDKI 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         856 LQDKKDGTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  813 V-AGQPVVLDVAAGGIDIASRKGER-PALTFITPLAAPGEEQRRRTKTGKSEFTTFVEIV 870
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  95 LQKHSTNKLAK-GLDSVE----NIDRKLGKASNVLSTLSSFLGTALAGIELDSLIKKGD- 148
                                                                                     43 DFIKAAD----ELGIARLABEPNHTETAKKSVDTVNQFL----SLTQTGIAISATKLEKF 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RGGDD---ILRGGLGLDTLYGEDGNDIFLQDDETVSDDIDGGAGLDTVDYSAMI----HPG
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Search completed: September 11, 2002, 09:00:12 Job time: 230 sec

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Maximum DB seq
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Copyright (c) 1993 - 2000 Comp
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                                                                                                                                                                                                                         DB
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               AAR54781
AAR86998
AAR76990
AAE04637
AAE04636
AAR10889
AAR42385
                                                                                                                                              AAB62110
AAW22159
AAY51412
                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Search time 75.59 Seconds (without alignments) 20.572 Million cell updates/sec
                                                                                                                                                                                                                         Description
                                                                                          Leukotoxin AppIIIA
Enterohaemorrhagic
Actinobacillus ant
                                                                                                                                                              M. bovis Dalton
ApxIIIB protein.
                 Leukotoxin 352 enc
Recombinant leukot
                                                      Pasteurella
                                                                        Pasteurella
                                                                                                                                                  pleuropneumonia
                                                                                                                                                                                                                                                                                                                                  printed,
                                                      haemol
                                                                        haemol
                                                                                                                                                                                    2d
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42 54 42 54	42 54 42 54								63	63		63	63	63	63		63	63	63	63	63	63		63	63	63		49 63		49 63	49 63
	.5 138		.7 956			-	-	-		_	-				-		6	-	6		6			6					.6 926		.6 924
⊳	18 AAW2/248 22 AAU37416	AAWC	AAYS	AAW2215	AAR1256															14 AAR43865			14 AAR34548		14 AAR34547		AAW03	15 AAR50291	14 AAR34545	12 AAR14482	14 AAR4237
			•	•	•		•						•			•							_			_					_
Haemolysin C-termi Staphylococcus aur	Staphylococcus aur	P. suis leukotoxin	<ul> <li>A. pleuropneumonia</li> </ul>	ApxIIC protein. A		Bovine IL-2/Pasteu	Chimeric protein #	Bovine IL-2/LKT ch	Bovine IL-2 - LKT	Bovine gamma-IFN/P	Chimeric protein #	Bovine IFNgamma/LK	⋗	A. pleuropneumonia	ApxIA protein. Ac	RH		0	PtxA protein of Pa	Leukotoxin protein		105kD PTX protein	Rotavirus VP4-leuk	Somatostatin-leuko	_		P. haemolytica tru	Recombinant leukot	Leukotoxin 352 pro	S	Recombinant leukot

### ALIGNMENTS

AAB62110;

AAB62110 standard; Protein;

927

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29-MAY-2001

(first entry)

Moraxella; antigen; immune response; infection; RTX toxin; vaccine; antibacterial; A subunit. M. bovis Dalton 2d RTX toxin A subunit. Novel Moraxella bovis antigen useful in compositions for raising immune response in an animal, has protease, lipase or hemolysin activity . Farn (CSIR ) COMMONWEALTH SCI & IND RES (UYME ) UNIV MELBOURNE. 31-AUG-1999; 31-AUG-2000; 2000WO-AU01048 08-MAR-2001. WO200116172-A1 Moraxella bovis. 2001-235092/24. DB; AAF57290. ŗ, Strugnell R, 99AU-0002571. Tennent J; ORG

leukot

0,

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RESULT
AAW22159
ID AAW2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local :
                                                   preparations are bacterial preparations comprising one or more isolated and purified strains of a microorganism that produces one or more RTX toxins, where the strains have at least one cell-associated RTX toxin. The preparations are used for production of vaccines for the prophylaxis and treatment of infectious diseases caused by microorganisms that produce RTX toxins, where the strains have been attenuated or
 pleuropneumoniae infection (swine pleuropneumonia). It h
that A. pleuropneumonia produces significant quantities
cell-associated RTX toxins when cultured under certain c
                                                                                                                                       AAW22151-W22161 represent A. pleuropneumoniae RTX (repeat in toxins) toxins. These sequence are encoded by the apxICA, apxIBD, apxIIAB'C, apxIIIABCD genes (see AAT73217-T73220), and can be expressed by microorganisms used in the present of the invention. The
                                          inactivated. The vaccines are preferably against Actinobacillus
                                                                                                                                                                                                                         Disclosure; Pages 107-110;
                                                                                                                                                                                                                                                      pleuro-pneumonia
                                                                                                                                                                                                                                                                      Preparations
- especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RTX toxin; apxICA gene; apxIBD gene; apxIIAB'C gene; apxIIIABCD gene; repeat in toxins toxin; cell-associated RTX toxin; vaccine production; therapy; A. pleuropneumoniae infection; swine pleuropneumonia.
                                                                                                                                                                                                                                                                                                                                                          MacInnes J,
                                                                                                                                                                                                                                                                                                                                                                                       (UYGU-)
                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CA2170839-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Actinobacillus pleuropneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RTX toxin; apxICA gene; repeat in toxins toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ApxIIIB protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW22159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW22159 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to new Moraxella bovis antigens and nucleic acid sequences encoding these antigenic polypeptides. The antigenic polypeptides and polynucleotides are useful for raising an immune response in an animal directed against Moraxella, preferably against M. bovis or M. catarrhalis, and for treating Moraxella infections. The present sequence represents the amino acid sequence of the A subunit of the RTX toxin from M. bovis Dalton 2d.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                 AAT73220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                927
                                                                                                                                                                                                                                                                   of microorganisms producing for production of vaccines a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                         Mallard B,
                                                                                                                                                                                                                                                                                                                                                                                       GUELPH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein; 1049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .08;
                                                                                                                                                                                                                                                                                                                                                       Ricciatti P,
                                                                                                                                                                                                                       151pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 77;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                       Rosendal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 22;
7.4e-05;
ches 0;
                                                                                                                                                                                                                                                                y cell-associated against swine
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                              It has been found
conditions, and
                                                                                                                                                                                                                                                                                RTX toxins
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AAY51412
ID AAY5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                     This invention describes a novel bacterial preparation (I) which comprises one or more isolated and purified strain(s) of a microorganism, cultured in tryptone yeast extract (TYE) broth, which produces one or more RTX toxins (belonging to the family of toxins referred to as Repeats in Toxins), where the strain(s) have at least one RTX toxin which is cell-associated. The products of the invention have immunostimulatory, antimicrobial, antiinflammatory, antiarthritic and antiabortive activity. The bacterial preparation may be used as vaccines for the prophylaxis and treatment of infectious diseases caused by strains of microorganisms which produce one or more RTX toxins. The infectious diseases are swine which produce one or more RTX toxins. The infectious diseases are swine to the prophylaxis and which produce one or more RTX toxins. The infectious diseases are swine to the produce one or more RTX toxins.
            pleuropneumonia, pneumonia, septicemia, nephritis and arthritis septicemia, nephritis, endocarditis and arthritis in piglets; sh
                                                                                                                                                                                                                                                             Bacterial preparation comprising microorganisms which produce a of the Repeats in Toxins (RTX) family, useful for treating swine pleuropneumonia, arthritis in swine, shipping fever and abortion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiinflammatory; antiarthritic; antiabortive; tre-
pleuropneumonia; septicemia; nephritis; arthritis;
shipping fever; abortion; whooping cough; sleepy for
                                                                                                                                                                                                                      Disclosure; Column 77-84;
                                                                                                                                                                                                                                                                                                                                                                              Mallard B,
                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAZ88587
                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US6019984-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RTX toxin; vaccine; Repeats in Toxins; immunostimulatory; antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A. pleuropneumoniae apxIIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         that the whole-cell protein composition of the cultures corresponds the whole-cell protein profiles obtained from cells recovered at necropsy from the pleural fluid of infected swine. Vaccination with bacterin prepared from heat-inactivated cultures having significant quantities of cell-associated RTX toxins give significant protection swine against challenge with homologous strains.
                                                                                                                                                                                                                                                                                                                                                                                                             (UYGU-) UNIV GUELPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Actinobacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 passive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY51412 standard;
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nes 10; Conserv
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                                                                                                                                                                                                                                                      and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunization;
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    abortion
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                                                                                                                                                                                                                                                   sleepy
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                                                                                                                                                                                                                                                     foal disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peritonitis;
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   cattle;
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71
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                                                                                                                                                                                                                   96pp; English
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Pred.
whooping
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                                                                                                                                                                                                                                                                                                                                                                           Ricciatti P;
 cough,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB
າ.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gastroenteritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treatment;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        foal disease;
            in piglets; shipping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        endocarditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pneumonia;
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                           in swine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   joint ill (purulent nephritis, arthritis) in foals; septicemia, polyarthritis and abortion in horses; and uninary infections, peritonitis, meningitis, and gastroenteritis. The bacterial preparations may also be used to prepare antibodies which may be used as a means of passive immunization. This sequence represents the Actinobacillus passive immunization apxilia protein described in the method of the
                                                                                                                                                                                                                                  05-NOV-1992;
03-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                              Key
Sequence
                                The AppIIIA gene having the sequence given in AAQ64827 was isolated from phage lambda clones yfc 26–28 and yfc 31–32 of a genomic library of A. pleuropneumoniae ser. 2. The gene encodes a novel
                                                                               Disclosure; Fig 3; 65pp; English.
                                                                                                      and as diagnostic reagents
                                                                                                                DNA encoding Actinobacillus pleuropneumoniae leukotoxin - used prepare prods. for use in vaccines for porcine pleuropneumonia
                                                                                                                                                     N-PSDB; AAQ64827.
                                                                                                                                                              WPI; 1994-167130/20
                                                                                                                                                                                     Chang Y;
                                                                                                                                                                                                                                                                     04-NOV-1993;
                                                                                                                                                                                                                                                                                           11-MAY-1994
                                                                                                                                                                                                                                                                                                                  W09409821-A
                                                                                                                                                                                                                                                                                                                                                    Domain
                                                                                                                                                                                                                                                                                                                                                                          Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Actinobacillus pleuropneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leukotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leukotoxin AppIIIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR54781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR54781 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                           (CORR ) CORNELL RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention.
                        eukotoxin
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nes 10; Conservative
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                       of A. pleuropneumoniae ser.
xin (sequence AAR54781).
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  1244
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AppIIIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                  92US-0972229.
93US-0072285.
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 Ą,
                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                         'label• transmembrane
                                                                                                                                                                                                                                                                                                                                                                label= transmembrane domain
                                                                                                                                                                                                                                                                                                                                                                                      abel=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        pleuropneumonia; vaccine; diagnostic.
                                                                                                                                                                                                                                                                                                                                                      587
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                                                                                                                                                                                                                                                                                                                                                                                     transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 58; DB 2
Pred. No. 0.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                         domain
                                                                                                                                                                                                                                                                                                                                                                                       domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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Query Match

75.3%;

Score

58;

DΒ

15;

Length 1244;

13-MAR-1996

(first entry)

AAR76990

AAR76990 standard;

protein;

127

A

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RESULT AAR86998
ID AAR86998
XX AAR8
XX AAR8
XX AAR8
XX AAR8
XX BENTE
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XX EENTE
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OS ESC!
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RESULT
AAR76990
ID AAR7
XX
AC AAR7
XX
DT 13-M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qγ
                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 71.4 Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enterohaemorrhagic E.coli (EHEC) associated with enterohaemorrhagic colitis, haemolytic uremic syndrome and mesenteric adenitis have been found to carry a hlyA gene and a hylB gene, separated by an intergenic region. The hly genes and the intergenic region are absent from bacteria not associated with these diseases and so
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                provide a useful target for detecting EHEC pathogens, serotype E.coli. The present sequence is that of the encoded by the EHEC hlyA gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EHEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enterohaemorrhagic Escherichia coli; virulent; EHEC; O157:H7 serotype; detection; probe; primer; hlyA gene; enterohaemorrhagic colitis; haemolytic uremic syndrome; mesenteric adenitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Columns 37-42; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US5475098-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enterohaemorrhagic E.coli hlyA gene product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR86998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR86998 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Entero:haemorrhagic E. coli (EHEC) nucleic acid sequences for probe and primer design for sensitive and specific detec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hall RH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli (enterohaemorrhagic)
                                                                                                                                                                                                                                  480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           920 frdifhgadgddll 933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 FNDIFHSGEGDDLL
                                                                                                                                                                                                                                                                                1 FNDIFHSGEGDDLL
                                                                                                                                                  6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ഗ
                                                                                                                                                                                                                                fndifhgadgndyi 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1996-048546/05
                                                                                                                                                                                                                                                                                                                                     Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT08098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ×
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  758
                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94US-0258188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94US-0258188
                                                                                                                                                                                                                                                                                     14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14
                                                                                                                                                                                                                                                                                                                                                             67.5%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              758
                                                                                                                                                                                                                                                                                                                                  Score 52; DB
Pred. No. 1.4;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ۲.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 0.21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ą
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                                                                                                                                                                                                                                                                                                                                                             DB :
                                                                                                                                                                                                                                                                                                                                                                                     17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ω
--
                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     esp. 0157:H7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of.
                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
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RESULT
AAE04637
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                   Matches
17-DEC-1999;
                                                       WO200144289-A2
                                                                         Synthetic
                                                                                                      animal
                                                                                                                                                                                                                                                                                                                                                      AAR76990 represents a repeat region of the lhaA (low homology to apply gene product which is a toxin component. The repeat region and full gene product are useful as the active ingredient in vaccines for the prophylaxis of Actinobacillus (Haemophilus) pleuropneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
Region
                  15-DEC-2000; 2000WO-CA01498
                                     21-JUN-2001
                                                                                  Pasteurella
                                                                                                                                                                                                                                                                                                                                                                                                                          A vaccine contg. a product of the LhaA gene as the active ingredient - for prophylaxis of Actinobacillus (Haemophilus) pleuropneumoniae infectious diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
                                                                                                                        Leukotoxin 50; lkt50;
                                                                                                                                          Pasteurella
                                                                                                                                                             10-SEP-2001
                                                                                                                                                                                AAE04637;
                                                                                                                                                                                                AAE04637 standard; Protein;
                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NISK ) NIPPON SEIBUTSU KAGAKU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JP07138185-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Actinobacillus
                                                                                                                                                                                                                                                                                                                                                 infectious (Ap1) diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ap1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Actinobacillus
                                                                                                               .mmunostimulant;
                                                                                                                                                                                                                                               15
                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                               1 FNDIFHSGEGDD
                                                                                                                                                                                                                    7
                                                                                                                                                                                                                                             ftdifhgakgdd
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1995-228639/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat;
                                                                                                    feed;
                                                                                                                                                                                                                                                                                  Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                       Page 8; 15pp;
                                                                                                                                                                                                                                                                                                                                127
                                                                                                                                        haemolytica modified
                                                                                  haemolytica
                                                                                                                                                                                                                                                                                  Conservative
                                                                                                     mutant;
                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vaccine;
99US-0172148
                                                                                                                                                                                                                                                                                                                                AΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93JP-0152264.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93JP-0152264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pleuropneumoniae
                                                                                                             antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note=
                                                                                                                                                                                                                                                                12
                                                                                                                                                                                                                                               26
                                                                                                                                                                                                                                                                                          63.6%;
66.7%;
                                                                                                     mutein.
                                                                                                                     respiratory disease; infection; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antigenic;
                                                                                                                                                                                                                                                                                                                                                                                                        Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "tandem repeat units
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    toxin repeat (RTX) region
                                                                                                                                                                                                450
                                                                                                                                                                                                                                                                                 Score 49; DB
Pred. No. 0.62
1; Mismatches
                                                                                                                                                                                                                                                                                  <u>..</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KENKYUSHO
                                                                                                             vaccine;
                                                                                                                                                                                                ΑĀ
                                                                                                                                       leukotoxin 50 (lkt50) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunisation; pneumonia;
                                                                                                                                                                                                                                                                                     DB .
า.62;
                                                                                                            transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZH
                                                                                                                                                                                                                                                                                                   16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                  Length 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acids"
                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                  appA)
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RESULT
AAE04636
DЪ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                       17-DEC-1999;
                                                                                                                                                                                                                         Pasteurella haemolytica
                                                                                                                                                                                                                                               animal feed; mutant; mutein.
                                                                                                                                                                                                                                                                                         Pasteurella haemolytica modified leukotoxin 66 (lkt66) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is Pasteurella (Mannheimla) haemolytica modified leukotoxin-50 (1kt50) protein. The modification comprise modified leukotoxin-50 (1kt50) protein. The modification comprise the removal of amino acids within the hydrophobic transmembrane domain of a full length leukotoxin protein. Modified leukotoxin sequences are used in vaccines to treat or prevent diseases assowith leukotoxin, e.g., respiratory disease, and Mannheimla infect (particularly M. haemolytica infection). In addition, the vaccin
                                                                            Lo RYC,
                                                                                                  (UYGU-) UNIV
                                                                                                                                            15-DEC-2000;
                                                                                                                                                                    21-JUN-2001
                                                                                                                                                                                         WO200144289-A2
                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                      Leukotoxin
                                                                                                                                                                                                                                                                                                                   10-SEP-2001
                                                                                                                                                                                                                                                                                                                                         AAE04636;
                                                                                                                                                                                                                                                                                                                                                              AAE04636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Fig 12; 70pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified leukotoxin polypeptide is useful in a vaccine to prevent or treat Mannheimia (Pasteurella) infection (particularly M. haemolytica infection), and disease associated with a leukotoxin, e.g., respiratory disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       is used to prepare a medicament. Furthermore, the plant transformed with modified leukotoxin sequences is fed to an animal such as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAD08976.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lo RYC,
                                                                                                                                                                                                                                                             mmunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ruminant,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYGU-) UNIV GUELPH OFFICE.
                                                                                                                                                                                                                                                                                                                                                                                                                      324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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                                                     2001-408470/43.
                                                                                                                                                                                                                                                                                                                                                                                                                    ndllhggkgddi
                                                                                                                                                                                                                                                                                                                                                                                                                               NDIFHSGEGDDL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001-408470/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 58.7; Conservative
                                                                           Shewen PE,
                                                                                                                                                                                                                                                                                                                                                              standard; Protein; 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to prevent or treat respiratory diseases
                                                                                                                                                                                                                                                                      66; lkt66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        450 AA;
                                                                                                  GUELPH
                                                                                                                                              2000WO-CA01498
                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                       99US-0172148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PE,
                                                                                                                                                                                                                                                           antibacterial; v
                                                                                                   OFFICE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.6%;
58.3%;
                                                                           Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lee
                                                                           RWH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RWH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
Pred.
                                                                         Hodgins
                                                                                                                                                                                                                                                                                                                                                              Ã
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hodgins
                                                                                                                                                                                                                                                           vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                      disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49;
No.
                                                                         Ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB
2.6;
                                                                                                                                                                                                                                                           transgenic
                                                                          Strommer
                                                                                                                                                                                                                                                                      infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strommer
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                         plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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Modified leukotoxin polypeptide is useful in a vaccine to prevent or treat Mannheimia (Pasteurella) infection (particularly M. haemolytica infection), and disease associated with a leukotoxin, e.g., respiratory

Claim 2; Fig disease

2

70pp;

English.

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RESULT AAR10889
ID AAR10889
ID AAR10889
ID AAR10889
ID AAR1
XX AAR1
XX LEUK
XX LKT;
XX PAST
XX O6-A
XX O6-A
XX O7-C
XX O7-C
XX O7-C
XX PAST
XX UYE
PA (UYE
XX PAST
PT VACC
XX PAST
XX PAST
PT VACC
XX PAST
CC LEUT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local 9
                          Plasmid pAA352 is derived from pAA114, a clone isolated from a genomic library of P. haemolytica. The protein, designated "new leukotoxin" or "LKT 352" is 98% homologous to authentic leukotoxin. LKT 352 and pref. antigenic fragments of it, can be used in vaccines to protect cattle from respiratory diseases. They can also be used to produce antibodies for immunoaffinity purificn. of further proteins. [Fig. contg. sequence v. poor]. see also AAR10890, AAR10909, AAR10910 and AAQ10783.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is Pasteurella (Mannheimia) haemolytica modified leukotoxin-66 (lkt66) protein. The modification comprises the removal of amino acids within the hydrophobic transmembrane domain of a full length leukotoxin protein. Modified leukotoxin sequences are used in vaccines to treat or prevent diseases associated with leukotoxin, e.g., respiratory disease, and Mannheimia infection (particularly M. haemolytica infection). In addition, the vaccine is used to prepare a medicament. Furthermore, the plant transformed with modified leukotoxin sequences is fed to an animal such as a ruminant, to prevent or treat respiratory diseases.
                                                                                                                                                                                                   Pasteurella haemolytica proteins and genes - vaccines to protect animals esp. cattle from e.g. pneumonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CA2014033-A
                                                                                                                                                                           Claim 13;
                                                                                                                                                                                                                                                                                                                 Acres
                                                                                                                                                                                                                                                                                                                                                                               07-APR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                            06-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                           07-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pasteurella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LKT; vaccine; antigen; respiratory disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR10889;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR10889 standard;
                                                                                                                                                                                                                                                                                                                                              (UYSA-) UNIV SASKATCHEWAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leukotoxin 352 encoded by plasmid pAA352.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            429 ndllhggkgddi 440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 NDIFHSGEGDDL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                 SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Conserv
                                                                                                                                                                                                                                                                     AAQ10272
                                                                                                                                                                        Fig
                                                                                                                                                                                                                                                                                                                 Babiuk LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     809
   924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        haemolytica Al strain B122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                        5; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                               89US-0335018.
                                                                                                                                                                                                                                                                                                                                                                                                            90CA-2014033.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63.6%;
58.3%;
                                                                                                                                                                                                                                                                                                                 Potter AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 49;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                               Lawman MJP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DΒ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     shipping fever pneumonia.
                                                                                                                                                                                                                    used for producing respiratory diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 608;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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747 ndllhggkgddi 758

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NDIFHSGEGDDL 13

Conservative

Mismatches

2

Indels

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Gaps

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RESULT AAR42385
Query Match
Best Local Similarity
7; Conserv
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Best Local Similarity
"hes 7; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-APR-1992;
04-JUN-1992;
04-JUN-1992;
04-JUN-1993;
29-MAR-1993;
29-MAR-1993;
29-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harland R. Rioux C,
                                                                                                                                                                                               The lppB gene protein was expressed in E. coli as a fusion to the Pasteurella haemolytica leukotoxin gene iktA coded for by plasmid pAA352. The llpB gene fragment was taken from pMS11. LppB can be used in vaccines for preventing or treating H. somnus infections, which cause thromboembolic meningo-encephalitis, septicaemia, arthaper and provincia is a company to the context of th
                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 11; 119pp; English.
                                                                                                                                                                                                                                                                                                                                                                    and corresp. DNA
                                                                                                                                                                                                                                                                                                                                                                                     Haemophilus somnus immunogenic proteins used in vaccines selected from haemin-binding protein, haemolysin, LppB an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1993-351733/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-APR-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-APR-1994
                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pneumonia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thromboembolic meningoencephalitis; septicaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR42385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR42385 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYSA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-OCT-1993.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10
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                                                                                                                                                              pneumonia in vertebrates. also AAR42370-86.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ51086.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , Pfeiffer
Theisen M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lktA
                                                                                                                      924 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       somnus; immunogenic; haemolysin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          haemolytica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                leukotoxin peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SASKATCHEWAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93US-0038288.
93US-0038288.
93US-0038719.
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92US-0893424.
92US-0893426.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene; haemin-binding protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13
                                      63.6%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63.6%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pontarollo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           924
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ω
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                                      Score 49; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from
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                                  DВ
3.7;
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5.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LppB; LppC;
mia; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ņ
                                                         Length 924;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 924;
                                                                                                                                                                                                                                                                                                                                                                                       LppB and LppC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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RESULT 12
AAR42378
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AAR42380
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XXXXXX
                                                                                                                                                      Query Match
Best Local
                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-JUN-1992;
04-JUN-1992;
29-MAR-1993;
29-MAR-1993;
29-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                                               The hmb gene encoding the haemin-binding protein was expressed in E. coli as a fusion to the Pasteurella haemolytica leukotoxin gene lktA coded for by plasmid pAA352. The hmb gene fragment was taken from pRAP504 and starts at the codon for the 33 rd amino acid residue of ORF1. The haemin binding protein can be used in vaccines for preventing or treating H. somnus infections, which cause thromboembolic
        19-APR-1994
                             AAR42378;
                                                AAR42378
                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 6; 119pp; English.
                                                                                                                                                                                                                                                                                                                                             and
                                                                                                                                                                                                                                     meningo-encephalitis,
                                                                                                                                                                                                                                                                                                                                                    Haemophilus somnus immunogenic proteins used in vaccines selected from haemin-binding protein, haemolysin, LppB an
                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAQ51082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9321323-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haemophilus somnus; immunogenic; haemolysin; LppB; LppC; thromboembolic meningoencephalitis; septicaemia; arthritis; pneumonia; lktA gene; haemin-binding protein; fusion protein.
                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                    See also
                                                                                                                                                                                                                              vertebrates
                                                                                                                                                                                                                                                                                                                                                                                                                            Harland
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYSA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-APR-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pasteurella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant
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                                                                                                    747
                                                                                                                                                                                                                                                                                                                                                                                                                 Rioux C,
                                                                                                              2 NDIFHSGEGDDL 13
                                                                                                                                                                                                                                                                                                                                            corresp. DNA
                                                                                                   ndllhggkgddi 758
                                                                                                                                                                                                                                                                                                                                                                                              1993-351733/44.
                                                                                                                                                                                                                                                                                                                                                                                                                            RJ,
                                                                                                                                            Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                 VINU
                                                standard; Protein;
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                                                                                                                                                                                               924
                                                                                                                                                                                                                                                                                                                                                                                                                 Theisen M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    leukotoxin
                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        haemolytica.
       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                            Pfeiffer
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SASKATCHEWAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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93US-0038288.
93US-0038719.
                                                                                                                                                                                               AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92US-0893424.
92US-0893426.
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                                                                                                                                                      63.6%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                            cc,
                                                                                                                                                                                                                                      septicaemia, arthritis
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                                                                                                                                                                                                                                                                                                                                                                                                                            Pontarollo RA,
                                                                                                                                           Score 49; DB
Pred. No. 5.7;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 924
                                                924
                                                                                                                                            ω
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                                                AA
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                                                                                                                                                      DB 14;
5.7;
                                                                                                                                                                                                                                                                                                                                                                                                                           Potter AA;
                                                                                                                                                                                                                                      and pneumonia
                                                                                                                                           2;
                                                                                                                                                               Length 924;
                                                                                                                                                                                                                                                                                                                                                    LppB and LppC,
                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pGCH4
                                                                                                                                                                                                                                      in
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                                                                                                                                          Gaps
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RESULT :
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                                                                                                                                                                                                                                           Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-APR-1992;
04-JUN-1992;
04-JUN-1992;
04-JUN-1993;
29-MAR-1993;
                                                                                                                                                                                                                                                                                                                         The hmb gene encoding the haemin-binding protein was expressed in E. coli as a fusion to the Pasteurella haemolytica leukotoxin gene lkth coded for by plasmid pAAS52. The hmb gene fragment was taken from pRAP501 and starts at the codon for the third amino acid residue of ORF1. The haemin binding protein can be used in vaccines for preventing or treating H. somnus infections, which cause thromboembolic meningor-encephalitis, septicaemia, arthritis and pneumonia in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haemophilus somnus; immunogenic; haemolysin; LppB; LppC; thromboembolic meningoencephalitis; septicaemia; arthritis; pneumonia; lktA gene; haemin-binding protein; fusion protein.
                            Pasteurella
                                                                                                               AAR14482;
                                                                                                                                   AAR14482 standard;
                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 5; 119pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                  and corresp. DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                          Haemophilus somnus immunogenic proteins used in vaccines selected from haemin-binding protein, haemolysin, LppB and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1993-351733/44.
N-PSDB; AAQ51081.
                                                Antigen; leukotoxin; vaccine;
                                                                     LKT352
                                                                                          15-JAN-1992
                                                                                                                                                                                                                                                                                                        See also AAR42370-86.
                                                                                                                                                                                                                                                                                                                   vertebrates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Harland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYSA-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09321323-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pasteurella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant leukotoxin peptide
                                                                                                                                                                                    747 ndllhggkgddi 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rioux C,
                                                                                                                                                        13
                                                                                                                                                                                                            N
                                                                                                                                                                                                           NDIFHSGEGDDL
                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Theisen
                                                                                                                                                                                                                                                                                   924 AA;
                          haemolytica
                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfeiffer
heisen M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     haemolytica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SASKATCHEWAN
                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93US-0038287.
93US-0038288.
93US-0038719.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92US-0865050.
92US-0893424.
92US-0893426.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93WO-CA00135
                                                                                                                                                                                                            13
                                                                                                                                    Protein; 926
                                                                                                                                                                                                                                           63.6%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ,
33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pontarollo
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                                                                                                                                                                                                                                         Score 49; I
Pred. No. 5.
                                                lktA
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                                                                                                                                    AA
                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RA,
                                                                                                                                                                                                                                           DB
5.7;
                                                                                                                                                                                                                                                    14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Potter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 plasmid
                                                                                                                                                                                                                               ?:
                                                                                                                                                                                                                                                    Length 924;
                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The LKT352 gene was prepd. as follows: lktA, an MaeI fragment contg. the gene was ligated into the SmaI site of pUC13 to form pAA179. From this, two constructs were made in the ptac-based vector, pGH432:lacI digested with SmaI. One, pAA342, contsined the entire MaeI fragment from lktA while the other, pAA345, contained the entire MaeI fragment. Clone pAA342 expressed a truncated leukotoxin peptide at high levels while pAA345 expressed full length leukotoxin at very low levels. The 3' end of the lktA gene of pAA345 was therefore ligated to StyI/BamHI digested pAA342 to yield pAA35 contg. the LKT352 sequence. The protein expressed from the vector can be used to prepare a subunit vaccine with other P. haemolytica antigens, e.g. fimbrial protein, plasmin receptor or 50K outer membrane protein. The vaccines can be used to paase a subunit vaccine with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     shipping
See also
                                                                                                                                                      Vector; LKT 352; flanking; recombinant; antigen; somatostatin;
gonadotropin releasing hormone; rotavirus viral protein 4;
carrier protein; lactation; reproduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vaccines for Pasteurella haemolytica infection in cattle - comprise sub-unit antigens from P haemolytica fimbrial protein, plasmin receptor, 50 K outer membrane protein and leukotoxin.
                                                                                                                                                                                                                                                                           AAR34545
                                                                                                                                                                                                                                                                                                   AAR34545 standard; Protein; 926 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 5; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-APR-1990;
16-OCT-1991;
14-OCT-1992;
                                          15-OCT-1992;
                                                                      29-APR-1993
                                                                                                                            Pasteurella haemolytica
                                                                                                                                                                                                                  Leukotoxin 352 produced from pAA352.
                                                                                                                                                                                                                                              23-AUG-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to protect cattle from respiratory diseases such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to the same position on gels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LKT352 is 98% homologous with authentic leukotoxin and migrates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Acres SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-OCT-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYSA-) UNIV SASKATCHEWAN
                                                                                                                                                                                                                                                                                                                                                                              747
                                                                                                                                                                                                                                                                                                                                                                                                         N
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ndllhggkgddi 758
                                                                                                                                                                                                                                                                                                                                                                                                         NDIFHSGEGDDL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 58.: 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fever pneumonia.
AAR14481, 83,84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bariuk LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            926 AA;
91US-0779171.
92US-0960932.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90US-0504850.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91WO-CA00170.
                                          92WO-CA00449.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83,84 and 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Potter AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 49; DB
Pred. No. 5.7;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lawman
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 12;
5.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MJP;
                                                                                                                                                                                                                                                                                                                                                                                                                                     2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 926;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pneumonia,
                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  esp.
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$\times CCCCCCCCCCCCCCCCCCCC\times T\times T\t
                                                                                     colonies were screened for their ability to produce leukotoxin by colonies were screened for their ability to produce leukotoxin by colonies were screened for their ability to produce leukotoxin by colonies were screened for their ability to produce leukotoxin by colonies were flactate dehydrogenase from the neutrophils. A 4kb crelease of lactate dehydrogenase from the neutrophils. A 4kb creament was obtd. Progressively larger clones were isolated by colonies was unjected to restriction enzyme digestion to yield two clones, one expressing truncated leukotoxin peptide at high levels and the other expressing truncated leukotoxin peptide at clow levels. The 3' end of the lkt gene from the full length clone was ligated to the truncated gene clone to yield plasmid pha352. The clone was used to produce chimeric proteins by gene fusion with an antigen coding sequence, e.g. the coding sequence of somatostatin, companion continuous sequence of companion with the colonies as a carrier protein to bring about a larger leukotoxin works as a carrier protein to bring about a larger antigens can regulate growth rate, lactation and reproductive efficiency. See also AAR34546-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in lambda gtl1 and pUCl3. Resulting clones were used to transform E coli and individual colonies were pooled and screened for reaction with serum from a calf which had survived a P. haemolytica infection and that had been boosted with a conc. culture supernatant of P.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene libraries of P. haemolytica Al (strain B122) were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 3; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gonadotropin releasing hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        comprises chimeric protein comprising leuco:toxin peptide homologous protein fused to antigen esp. somatostatin or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYSA-) UNIV SASKATCHEWAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunological carrier system with enhanced immunogenicity
926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Potter AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Redmond MJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [F]
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Matches Query Match Best Local 2 NDIFHSGEGDDL 13 7; Conserv Conservative 63.6%; 58.3%; Score 49; DB Pred. No. 5.7; 3; Mismatches ω DB 5.7; 14; Length 926; Indels 0 Gaps 0;

Q

RESULT AAR50291 밁 06-OCT-1994 AAR50291; AAR50291 standard; Protein; 747 15 ||: | |:||: ||ndllhggkgddi 758 (first entry) 926 AA

LKT352. Vaccine; regulated membrane protein; protein; OMP; Haemophilu
leukotoxin; Pasteurella Haemophilus somnus; Asteurella haemolytica; Recombinant leukotoxin from plasmid pAA352

Pasteurella haemolytica Al (strain B122)

ID XXX AC 03-JAN-1994

29-JUN-1993; 93CA-2099707

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Page 8
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Вþ
                                                                                                                    Qy
                                                                                                                                                                                                                                                                                                                                              A vaccine comprising an outer membrane protein (OMP) extract of Haemophilus somnus enriched with iron regulated proteins is new. The vaccine pref. further comprises an immunogenic leukotoxin polypeptide, esp. an immunogenic pasteurella haemolytica leukotoxin hamologous to LKT352. Example 1.2 describes the prodn. of p. haemolytica recombinant leukotoxin from pAA352.

Two expression constructs were made. One, pAA342, contained the contained the entire lktA gene, while the other, pAA345, contained the entire lktA gene, pAA342 expressed a truncated leukotoxin peptide at high levels, while pAA345 expressed full 1. Leukotoxin peptide at high levels. Therefore, the 3' end 1. Conference was ligated into pAA342, yielding plasmid pAA352.

LEM352 or new leukotoxin is 98% homologous to authentic
earch completed: September 11, 2002, 08:58:48
ob time: 192 sec
                                                                                                                                                        Query Match 63.6%;
Best Local Similarity 58.3%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haemophilus sommus outer membrane protein extract - enriched with iron-regulated proteins, opt. contg. leuco:toxin antigens, for use as vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1994-092909/12.
N-PSDB; AAQ44760.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-JUL-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 5; Fig 5; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Harland RJ, Potter AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYSA-) UNIV SASKATCHEWAN
                                                                                                                                                                                                                                                                              leukotoxin.
NB: the protein sequence in Fig 5 comprises 926 amino acids, however this protein is described in the text as having 931 amino acids.
                                                                                                                                                                                                                                               Sequence
                                                                                     2 NDIFHSGEGDDL 13
||: | |:||:
747 ndllhggkgddi 758
                                                                                                                                                                                                                                                 926 AA;
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                                                                                                                                                             ω.
                                                                                                                                                           Score 49; DB 15;
Pred. No. 5.7;
3; Mismatches 2
                                                                                                                                                               2
                                                                                                                                                                                               Length 926;
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
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                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
2782.4
817.6
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1: /SIDS1/gcgdata//
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  99.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             September 15, 2002, 09:00:42; Search time 433.33 Seconds (without alignments) 11030.600 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1736436 seqs, 858457221 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
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2784
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   atgtccaatataaatgtaat.....ttttggctccaagtgtttag 2784
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/SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001b.DAT:*
/SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001b.DAT:*
/SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
                                                                                                                                                                                                                                                Length DB
                                                     2861
2794
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AAF57290
AAQ10727
AAT60032
AAA7483
AAQ41322
AAQ41323
AAQ41323
AAQ14238
AAQ41317
AAQ44760
                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.5
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3472872
                                                                                                                   M. bovis Dalton 2d
Leukotoxin 352 ge
Chimeric protein #
Bovine IL-2/Pasteu
                                                                                                                                                                                                                                           Description
  Recombinant leukot
                         LKT352 gene. I
Leukotoxin 352
                                                                       Rotavirus VP4-leuk
                                                                                                 GnRH-leukotoxin ge
                                                Past
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41.8 12.	12.	43.2 12.	43.2 12.	71.2 13.	14.	66.2 16.	6.2   16.	73.8 17.	8.8 17.	.8 17.	22.	22.	22.	27.	27.	75 27.	.4 28.	.6 29.	29.	.8 29.	L3 29.	14 29.	14 29.	14 29.	814 29.	14.4 29.	14.4 29.	14.4 29.	14.4 29.	14.4 29.	14.4 29.	14.4 29.	4.4 29.	14.4 29.
1635		2088	2088	1359	2278	3240	3072	1827	3762	3762	7721	7721	4008	3831	4731	4731	3848	4203	2794	.2838	7183	7184	3879	3311	3311	3977	3887	3646	3229	3229	3229	2934	2934	2794
19 AAV61532	AAZ46	AAZ5570							AAZ8858										.7 AAT37179						AAQ2277	AAQ5108	AAQ5108	AAQ5108	AAA7248	AAT6003	AAQ5421	AAV6153	AAT3717	AAV615
Nucleic acid encod	Gonadotropin relea		Nucleic acid encod	Pasteurella haemol	Enterohaemorrhagic	(low	LhaA (low homology	Pasteurella haemol	A. pleuropneumonia	kICA gene. Act	A. pleuropneumonia	ApxIIIABCD gene.	Leukotoxin AppIIIA	appCA region encod	~	pxIIAB′	P. suis leukotoxin	Leukotoxin genes.	P. haemolytica leu	Somatostatin-leuko	Sequence encoding	ptx gene of Pasteu	nixc	IL-2/LK	IL-2 -		pGCH4	pcrR28 wh	amma-IFN/	Chimeric protein #	e IFNga	acid enco	-GnRH fusi	Nucleic acid encod

# ALIGNMENTS

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                        08-MAR-2001.
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                                                                                                                                                   Moraxella
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                                                                                                                                                                    Moraxella; antigen; immune response; infection; RTX toxin; vaccine; antibacterial; ds.
                                                                                                                                                                                          M. bovis Dalton 2d RTX toxin A subunit encoding DNA
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                                                                                                                                                                                                           (first entry)
                                                                                                                          Location/Qualifiers 232..3015
                                                                        /note= "partial coding region of RTX toxin 3080..3250
                                                                                                 /product= "RTX toxin A subunit"
1..195
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                                                         "partial coding region of RTX toxin B subunit"
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                             tcacagttagcaaagttaggttctactatatcgcaggctaaaggcttctctaatatagga
                                                                                                                                                                                                                                                                                                                                                                        ention relates to new Moraxella bovis antigens and nucleic actes encoding these antigenic polypeptides. The antigenic tides and polypucleotides are useful for raising an immune in an animal directed against Moraxella, preferably against sor M. catarrhalis, and for treating Moraxella infections. The sequence represents the nucleotide sequence of the A subunit toxin from M. bovis Dalton 2d.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
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22-AUG-1990;
16-OCT-1991;
                                                                                                                                                                                       IFN), linked to at least one RTX toxin epitope (preferably the sequence shown in AAW13865). The RTX toxin used to provide the epitope sequence is preferably a leukotoxin, especially the full-length Pasteurella haemolytica leukotoxin. Alternatively, the leukotoxin is a truncated leukotoxin lacking leukotoxic activity, especially LKT352. The chimeric proteins can be used for the production if vaccines against respiratory diseases such as pneumonia, particularly fibrinous pneumonia caused by P.haemolytica, including shipping fever in cattle.
                                                                                                                                                                                                                                                                                                                                                                        AAT60032 and AAT60033 represent the coding sequences for immunogenic chimeric proteins of the invention. This sequence represents a chimeric protein containing the bovine interleukin-2 (II-2) sequence and a leukotoxin sequence. The chimeric proteins of the invention comprise a cytokine, selected from interleukin-2 (II-2) and gamma interferon (gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            interleukin-2; IL-2; gamma interferon; gamma Pasteurella haemolytica; LKT352; respiratory fibrinous pneumonia; cattle; therapy; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bovine IL-2; interleukin-2; leukotoxin; LKT; respiratory disease; pneumonia; shipping fever; cattle; livestock; anti-Pasteurella vaimmunogen; ds.
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                                      Vaccine for stimulating immunity age protein comprising gamma-interferon Pasteurella haemolytica -
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Best Local Similarity 60.1%;
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Pred. No. 1.3e-170;
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                                                                                                                                                                              Oligonucleotides contg. sequences from bovine Rotavirus viral protein 4 (VP4) gene were constructed on a Pharmacia Gene Assembler using standard phosporamidite chemistry. The oligonucleotides were annealed and ligated into vector pAA352 (contg. the Pateurella heamolytica leuko-toxin gene) which had been digested with BamHI. The ligated DNA was used to transform E. coli strain MH3000. Transformants contg. the oligonucleotide inserts were identified by restiction endonuclease mapping and the recombinant plasmid designated pAA501. The chimeric protein produced from the plasmid works to bring about a larger immune response than the antigonalone, i.e. the leukotoxin works as a carrier protein.
                                                                                                                                                                                                                                                                                                                                     Immunological carrier system with enhanced immunogenicity comprises chimeric protein comprising leuco:toxin peptide homologous protein fused to antigen esp. somatostatin or gonadotropin releasing hormone
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14-OCT-1992;
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                                                                                                                                              Sequence 2861 BP; 947
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                                                                                                    The LKT352 gene was prepd. as follows: lktA, an MaeI fragment contg. the gene was ligated into the SmaI site of pUCl3 to form pAA179. From this, two constructs were made in the ptac-based vector, pGH32:lacI digested with SmaI. One, pAA342, consisted of the 5' AhaIII fragment from lktA while the other, pAA345, contained the entire MaeI fragment. Clone pAA342 expressed a truncated leukotoxin peptide at high levels while pAA345 expressed the lktA gene of pAA345 was therefore ligated to Styl/BamHI digested pAA342 to yield pAA352 contg: the LKT352 sequence. The protein expressed full from the vector can be used to prepare a subunit vaccine with other P. haemolytica antigens, e.g. fimbrial protein, plasmin receptor or 50K outer membrane protein. The vaccines can be used to proteir cattle from respiratory diseases used a neumonia esa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vaccines for Pasteurella haemolytica infection in cattle - comprise sub-unit antigens from P haemolytica fimbrial protein, plasmin receptor, 50 K outer membrane protein and leukotoxin.
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hemolytica to increase anti-leukotoxin antibody levels. Positive colonies were screened for their ability to produce leukotoxin by incubating cell lysates with bovine neutrophils and measuring the release of lactate dehydrogenase from the neutrophils. A 4kb fragment was obtd. Progressively larger clones were isolated by chromosome walking to isolate full length recombinants of ca. 8kb, in pAA114. The clone was subjected to restriction enzyme digestion to yield two clones, one expressing truncated leukotoxin peptide at high levels and the other expressing truncated leukotoxin at low levels. The 3' end of the 1ktA gene from the full length clone was ligated to the truncated gene clone to yield plasmid pAA352. The clone was used to produce chimeric proteins by gene fusion with an antigen coding sequence, e.g. the coding sequence of somatostatin, gonadotrophin releasing hormone or rotatics viral protein 4, i.e. leukotoxin works as a carrier protein to bring about a larger immune response than the antigen alone. Immunisation with these
                                              immune response than the antigen alone. antigens can regulate growth rate, lacta efficiency. See also AAQ41318-23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in lambda gtll and pUCl3. Resulting clones were used to transform E coli and individual colonies were pooled and screened for reaction with serum from a calf which had survived a P. haemolytica infection and that had been boosted with a conc. culture permatant of P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       comprises chimeric protein comprising leuco:toxin peptide homologous protein fused to antigen esp. somatostatin or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene libraries
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[F]

Query Match Best Local Similarity Matches 1538; Conserv Conservative 29.3%; Score 814.4; Pred. No. 1.8e
0; Mismatches 0 4; DB 14; 1.8e-170; 956; Indels Length 2794 60; Gaps

9

Sequence

2794

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487 C;

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G;

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other;

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and reproductive

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380 cgggtatagaacttgattctttaatcaaaaaaggtgatgctgcacctgatgcttttggcta ctggaatggatttagatgaggccttacagaa---taacagcaaccaacatgctcttgcta 436 466

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RESULT 9
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ID AAO44760 standard; DNA; 2794 BP.
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DT 06-OCT-1994 (first entry)

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Best Local Similarity 60.3
Matches 1538; Conservative
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                                                                                                                                                                                                                                                                                                                                                                       polypeptide, esp. an immunogenic Pasteurella haemolytica leukotoxin homologous to LKT352. Example 1.2 describes the prodn. of P. haemolytica recombinant leukotoxin from pAA352.
                                                                                                                                                                                                                                                                                                                                                                                                                  A vaccine comprising an outer membrane protein (OMP) extract Haemophilus somnus enriched with iron regulated proteins is no The vaccine pref. further comprises an immunogenic leukotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haemophilus somnus outer membrane protein extract
enriched with iron-regulated proteins, opt. contg
leuco:toxin antigens, for use as vaccine
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                   The present sequence represents a recombinantly produced or chemically synthesised nucleic acid encoding leukotoxin 352 (LKT 352), derived from the lktA gene that is present in the plasmid pAA352. This gene produces a truncated protein that has an estimated molecular weight of about 99 kDa and lacks the cytotoxic portion of the molecule. Thus this gene has a higher expression level than that of the full-length molecule. This can be used in the construction of a chimeric protein that comprises a leukotoxin polypeptide, several multimers, and a GRH sequence. The chimeric protein can be used as a vaccine to help reduce the incidence of mammary tumours in a mammalian individual.
                                                                                                                                                                              Chimeric protein of leukotoxin and gonadotropin releasing useful for, e.g. preparation of vaccines for reduction of of mammary tumours in mammals
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P-PSDB;
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Query Match
Best Local S
Matches 1538
                                                                                                                                                                                                                                                                                                                      This sequence encodes a fusion between bovine gamma interferon (IFNgamma) and Pasteurella haemolytica leukotoxin (LTK). The leukotoxin gene, ltkA, was isolated from a gene library of P. haemolytica by chromosome walking. Immunogenic fusion proteins such as this can be used in vaccine compositions. It can also lused to raise mono- and polyclonal antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                  leukotoxin
antibodies
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                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunogenic fusion proteins of gamma-interferon and immunogenic
leukotoxin - used in vaccines and to raise monoclonal and polyc.
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(UYSA-) UNIV
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16-OCT-1991;
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nes 1538; Conser
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                                                                                                                                                                                                     caaagtctggattaaaaaatctttacttggctattcccaaagat-----tatgatccgc 106
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DB; AAR52748.
            aaaaacattctaccaataagttagccaaagggttagacagtgtagaaaatattgatcgta
                                                                                                                                           aacaaggtaatggtttacaggatttagtcaaagcggccgaagagttggggattgaggtac
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agaaa--
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                                                                                                                                                                                                                                                                                                                                                                                                         Fig
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                                                                                                                                                                                                                                       Conservative
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tibody; ds.
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Pred. No. 1.9e-170;
D; Mismatches 956;
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δÃ DЪ VΩ 뮹 VΩ Дy В δÃ Вþ δÃ Вþ γQ qq νQ DЬ δÃ 뫄 Qy Ъ ρ Вb δõ В Qy Вр Qy Ъ ŶΩ δ В Qγ Ър В Qy Db Qy 1424 1304 1217 1244 1157 1184 1097 1124 1037 1064 1277 1004 977 917 944 857 884 824 677 617 644 557 797 737 764 704 587 497 527 437 467 380 407 ctgagctaaataaagagttggaagctgaacgtgttattgcaatcacccaacaacgttggg aagcttatgcagatgcttttgaagatggcaagaaagttgaagctggttccaatattactt ataacaacattggtgatttagctggtattagccgtttaggtgaaaaagtccttagtggta ataataatattggtgagttagcaggtattaccaaattgggtgaacgcattaagagcggaa ctaaccgtttacaaggtaaaattttagagtgggaaaaggcaaaatggcggtcagaactatt ggactattgatgcatcggttactgcaattaataccgcattggccgctattgctggtg gtactattgaagcttcattaactacaattagtacggcattaggtgcagtttctgctggtg aattccgaaaatttggctatgatggggatcatttattggctgaatatcagcgtggtgtgg catttatgaatgcagcagataaattcaatcatgctaatgctcttgatgagtttgcaaaac ctactggtgctgttgctgctttaattacttcatcgattatgttggcaattagtcctttgg atgcatcgactggcaaaaaagttgctgcaggttttgaattaagcaatcaagttattggta tgaacttaaacaaagagttacaggcagaacgtgtcatcgctattactcagcagcaatggg ttgataaaaggctatgattctcgttatgctgcttatttagctaataacttaaaatttttgt tgtctgctgctgcagccggctcggttattgcttcaccgattgccttattagtatctggga tttccgctgctgctgtaggatctgctgttggtgcaccgattgcactattagttgcaggtg gctttaaaaaattaggctatgacggagataatttattagcagaatatcagcggggaacag caactgggcctgtggctttaattgcttctactgtttctctttgcgattagcccattag atgcttcaacagctaaaaaagtgggtgcgggttttgaattggcaaaccaagttgttggta tggaaataattactggtttgctatcaggcatttctgcaggctttgctttagcggataaaa ttgaagcattttcttcacagttagcaaagttaggttctactatatcgcaggctaaaggct ttgaaaatggttacgatgcccgttatcttgcgaatttacaagataatatgaaattcttac caaataaaattcataacaaaattgtagaatgggaaaaaaataatcacggtaagaactact catttgccggtattgccgataaatttaatcatgcaaaaagtttagagagttatgccgaac tagatgttatctcagggctattatcgggcgcaacagctgcacttgtacttgcagataaaa tagggactttaggagacaaactcaaaaatatcggtggacttgataaagctggccttggtt ttgacgaatttggtgagcaaattagtcaatttggttcaaaactacaaaatatcaaaggct aagctggcttggagctaacaaattcattaattgaaaatattgctaattcagtaaaaacac ctggaatggatttagatgaggccttacagaa---taacagcaaccaacatgctcttgcta cgggtatagàacttgattctttaatcaaaaaaggtgatgctgcacctgatgctttggcta 1276 1216 1096 1123 1036 1003 916 943 856 796 883 823 763 676 703 616 643 556 586 496 466 379 406

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QΥ Вb Qy Дδ QY ДЪ Qy Ър QΥ Ъ Ωy 밁 Qy В QΥ Вþ Qy Qy Дb 밁 DЬ DЪ Qy δÃ Ωy Ър Qy В Qy ₽ Qy 밁 Qy Ъ Qy B 2408 2183 2051 1994 1943 1874 1817 1757 2423 2351 2291 2303 2231 2171 2123 2063 1934 1883 1697 1724 2003 1637 1577 1397 1664 1604 1517 1544 gcaaaaaagagaaagtgaccattcaaaactggttccgagaggctgattttgctaaagaag atcattcaggtagtattaacataccaagatggtacataacatcaaaatttacaaaa ----caaatatatctgatattatgattgaacgtaccaaagagggtattatagttaaacgaaatg gcgatggtaatgatattattaccgattctgacggcaatgataaattatcattctctgatt gtgatggtaatgatactttgtacgatggcacgggcaatgataaattagcatttgcagatg gtaaaggcaacgacctattacacggtggcaagggcgatgatattttcgttcaccgtaaag gttctggtgatgatgtattaaattggtggtgctggtaatgatgtctatatctttcggaaag tattccatagtggtgaaggtgatgatttactcgatggtggtgctggtgacgaccgcttgt gtcatagcaataaccagcaccatg---ccggttattacaccaaagataccttgaaagctg gtgattatgaattaagaaaagttgggtatggttatcagtctaccgataatttgaaatcag acgaagtgacttcaacccataccgcattagtgggcaaccgtgaagaaaaaatagaatatc atgaagttgtgaagcgtcaagaaaccaaggtgggtaaacgtactgaaactatccagtatc aagagaccgagcaaggtagttataccgtaaatcgtttcgtagaaaccggtaaagcactac gtgcaacagaagcaggcagttatacagttaatcgtaaggttgctcgaggtgatatctacc acgatcgtgtcttctatagtaaagacggaggatttggtaatattactgtagatggtacga  $\verb|atggtgcagcaagttctacctttgatttaactaacgttgttcagcgtattggtattgaat|$ atggagaggctagttctaaattagatttctctaaagttattcagcgtgtagccgagacag cgaacttaaaagatttaacatttgaaaaagttaaaca---taatcttgtcatcacgaata ttggtggtaaaggcgatgatattctcgatggtggaaatggtgatgattttatcgatggcg cctttaacggtggtgatggtgtcgatactattgacggtaacgacggcaatgaccgcttat acgaccgagttcactatag---ccgtggaaactatggtgctttaactattgatgcaacca aaggtgatgacaacgtatttgttggttctggtacgacggaaattgatggcggtgaaggtt ctggcaatgacgatatctttgttggtcaaggtaaaatgaatattgatggtggagatggac gtaaatatgaatatattaccaagctcaatattaaccgtgtagatagctggaaaattacag tggatgctaaaactggtatcatagacattagtaattcaaatgggaaaaaacgcaagcgt tagacaatgctggaaatgtaactaaaaccaaagaaacaaaattattgccaaacttggtg tcttattcagaacgccattattgacgccgggaacagagcatcgtgaacgcgtacaaacag tgcatttcacttcgcctttgttaaccagcaggaactgaatcacgttgaacgtttaactaatt tggattcggcaaacggtattattgatgtgagtaattcgggtaaagcgaaaactcagcata ttatcaaagtaataaaacagatcataaaattgagcaactaattggtaaagatggta ģ 2407 2302 2230 2242 2170 2110 2122 2062 1993 2002 1933 1942 1873 1882 1816 1822 1756 1762 1696 1723 1636 1576 1516 1543 1456 2050

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AAT60033
ID AAT600
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22-AUG-1990;
16-OCT-1991;
                                                                                                                                                                    AAT60032 and AAT60033 represent the coding sequences for immunogenic chimeric proteins of the invention. This sequence represents a chimeric protein containing the bovine gammainterferon (gamma IFN) sequence and a leukotoxin sequence. The chimeric proteins of the invention comprise a cytokine, selected from interleukin-2 (IL-2) and gamma IFN, linked to at least one RTX toxin epitope (preferably the sequence shown in AAW13865). The RTX toxin used to provide the epitope sequence is preferably a leukotoxin, especially the full-length Pasteurella haemolytica leukotoxin. Alternatively, the leukotoxin is a truncated leukotoxin lacking leukotoxic activity, especially LKT352. The chimeric proteins can be used for the production if vaccines against respiratory diseases such as pneumonia, particularly fibrinous pneumonia caused by P. haemolytica, including shipping fever in cattle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RTX cytotoxin; cytokine; immunogen; chimeric protein; cytokine; vaccine; interleukin-2; IL-2; gamma interferon; gamma IFN; leukotoxin; pneumonia; Pasteurella haemolytica; LKT352; respiratory disease; shipping fever;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unic chimeric proteins comprising useful in vaccines, esp. against
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                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GEIGY CANADA LTD SASKATCHEWAN.
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90US-0571301.
91US-0777715.
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IL-2; gamm
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22-JUL-1996;
22-AUG-1990;
16-OCT-1991;
        Vaccine for stimulating immunity against pneumonia protein comprising gamma-interferon and leukotoxin Pasteurella haemolytica -
                                                                                                  (UYSA-)
(CIBA )
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                                                 P-PSDB;
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DB; AAB21074.
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GEIGY CANADA
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96US-0681479.
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Best Local Similarity 60.2
Matches 1538; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  used in an anti-Pasteurella vaccine composition. Pasteurella species, especially Pasteurella haemolytica, are responsible for respiratory diseases in a range of agricultural animals, most particularly cattle, but also sheep, pigs, horses and fowl. Shipping fever is the most economically important respiratory disease associated with Pasteurella species, affecting .5-30% of exposed cattle and resulting in a 2-5% mortality rate in the exposed population. The vaccine composition of the invention is is useful for preventing or ameliorating respiratory diseases such as pneumonia, particularly shipping fever
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3229 BP; 1085 A; 571 C; 690 G; 883 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents DNA encoding a fusion protein comprising bovine gamma-interferon (gamma-IFN) and Pasteurella haemolytica leukotoxin (LKT). The fusion protein is immunogenic, and may be
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                                                                       atgcatcgactggcaaaaaagttgctgcaggttttgaattaagcaatcaagttattggta
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2528 agcggatcacctcaaagcaagttgatgatcttat 2561
                                                        2468 tgcctaattataaagcaactaaagatgagaaaatcgaagaaatcatcggtcaaaatggcg 2527
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                                                                                                                                                                                                                                                                                                                                plasmid pAA352 is derived from pAA114, a clone isolated from a genomic library of P. haemolytica. The prottain, designated "new leukotoxin" or "LKT 352" is 98% homologous to authentic leukotoxin. LKT 352 and pref. antigenic fragments of it, can be used in vaccines to protect cattle from respiratory diseases. They can also be used to produce antibodies for immunoaffinity purificn. of further proteins. [Fig. contg. sequence v. poor].

See also AAR10890, AAR10909, AAR10910 and AAQ10783.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-APR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR10889
                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 13; Fig 5; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pasteurella haemolytica proteins vaccines to protect animals esp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1991-000097/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Acres SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYSA-) UNIV SASKATCHEWAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-OCT-1990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CA2014033-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pasteurella haemolytica Al strain B122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LKT; vaccine; antigen; respiratory disease; shipping fever pneumonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leukotoxin 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR10889 standard; Protein; 924 AA
                    Pasțeurella haemolytica
                                                                                                                              AAR42385
                                                                                                                                                   AAR42385 standard; Protein; 924
WO9321323-A
                                         pneumónia; lktA gene; haemin-binding
                                                  Haemophilus somnus; Ammunogenic; haemolysin; LppB; LppC; thromboembolic meningoencephalitis; septicaemia; arthritis;
                                                                                    Recombinant
                                                                                                          19-APR-199
                                                                                                                                                                                                         || |||||||||||
422 fllnlnkelgae 433
                                                                                                                                                                                                                                1 FLSELNKELEAE 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         pneumonia.
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9; Conserv
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                                                                                                                                                                                                                                                                                                               924 AA;
                                                                                                                                                                                                                                                       Conservative
                                                                                    leukotoxin peptide from plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                  75.4%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   by plasmid pAA352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Potter AA,
                                                                                                                                                                                                                                                       ۲,
                                                                                                                                                                                                                                                                  Score 43;
Pred. No.
                                                                                                                                                     AA
                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and genes - used for producing cattle from respiratory diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lawman MJP;
                                          protein; fusion protein
                                                                                                                                                                                                                                                                 DB
52;
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                                                                                      pCRR28
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04-JUN-1992;
04-JUN-1992;
04-JUN-1993;
29-MAR-1993;
29-MAR-1993;
04-JUN-1992;
04-JUN-1992;
29-MAR-1993;
29-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The lppB gene protein was expressed in E. coli as a fusion to the Pasteurella haemolytica leukotoxin gene lktA coded for by plasmit pAA352. The llpB gene fragment was taken from pMS11. LppB can lused in vaccines for preventing or treating H. sommus infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haemophilus somnus immunogenic proteins used in vaccines selected from haemin-binding protein, haemolysin, LppB and LppC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB;
                                                                                                                                                  Haemophilus somnus; immunogenic; haemolysin; Lpp8; LppC; thromboembolic meningoencephalitis; septicaemia; arthritis; pneumonia; lktA gene; haemin-binding protein; fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                      and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 11; 119pp; English
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                                                                                                                                                                                                                                                                 AAR42380 standard; Protein; 924 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               which cause thromboembolic meningo-encephalitis, septicaemia, arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1993-351733/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYSA-) UNIV
                                           09-APR-1992;
                                                                 05-APR-1993;
                                                                                     28-OCT-1993
                                                                                                          WO9321323-A
                                                                                                                              Pasteurella haemolytica.
                                                                                                                                                                                            Recombinant leukotoxin peptide (split) from plasmid pGCH4
                                                                                                                                                                                                                    19-APR-1994
                                                                                                                                                                                                                                                                                                                       424
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fllnlnkelgae 435
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                                                                                                                                                                                                                                                                                                                                                                                                                       924 AA;
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heisen M;
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93US-0038287.
93US-0038288.
93US-0038719.
92US-0893424.
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75.0%;
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52;
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Copyright (c) 1993 - 2000 Comp
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AZ596050 SP_1031_A
AZ550256 ENTEV58TR
BH149983 ENTOP93TF
AL166032 Tetraodon
AZ528485 ENTCM64TF
AZ676218 ENTKE36TR
BH139532 ENTNC88TF
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         AZ676218
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## ALIGNMENTS

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                                                                                                                                                                                                                                                               J. Infect. Dis. (2001) In press
Contact: Bahrani-Mougeot FK
Department of Medicine-Division of
University of Maryland
MSTF Rm 9.00 -10 S. Pine St., Balti
Tel: 410-706-7560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                2b11-594, DNA sequence.
AF307788
AF307788.1 GI:12250179
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                                                                                                                                                                                                                            Class: unknown
                                                                                                                                                                                                                                                                                                                                                                Bahrani-Mougeot,F.K., Pancholi,S., Daous Identification of putative urovirulence
                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision;
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                                                                                                                                                                                                                                         fbahrani@umaryland.edu
                                                                   urovirulence
130 c
                                                                                               /clone_lib="Escherichia coli CFT073"
/note="uropathogenic; isolated based
hybridization with Escherichia coli
                                                                                                                                         /db_xref="taxon:562"
/clone="2b11-594"
                                                                                                                                                                     /organism="Escherichia
/strain="CFT073"
                                                                                                                                                                                                            ocation/Qualifiers
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No. 4.4e-12;
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AUTHORS
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ENTEK30TR Entamoeba histolytica
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Entamoeba histolytica
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                                                                                                                                                                                                                                                                                                                                                                                            Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2000)
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Fax: 301 838 3543
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Brendan J Loftus
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                                                                                                                                                                                                                                                                      Class: shotgun
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                                                                                                                                                                                                                                                                                                           DNA library
                                                                                                                                                                                                                                                                                                                             Clones are derived
                                                                                                                                                                                                                                                                                                                                            Email: bjloftus@tigr.org
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quality sequence stop;
Location/Qualifiers
/Clone_lib="Entamoeba histolytica Sheared DNA" note="Vector: pHOS1; Site_l: Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from broth cultures of E. histolytic using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a
                                                                                                                                            /organism="Entamoeba histolytica"
/strain="HM1:IMSS"
/db_xref="taxon:5759"
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Matches 323; Conserv
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genomic,
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                             ENTDV54TR Entamoeba histolytica Sheared DNA Entamoeba histolytica
                                               AZ551618
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              DNA sequence
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Pred. No. 1.7e-06;
0; Mismatches 401;
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0208
Fax: 301 838 3543
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High quality sequence stop: 838
Location/Qualifiers
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Determination of clone end sequences from Entamoeba histolytica
HM1:IMSS sheared DNA library
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//clone_lib="Entamoeba histolytica Sheared DNA"
//note="Vector: pHOS1; Site_l: Bit I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
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Fax: 301 838 3543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Loftus, B., Van Aken, S. and Fraser, C. Determination of clone end sequences HM1: IMSS sheared DNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: bjloftus@tigr.org
Clones are derived from
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Tel: 301 838
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/clone_"Vector: pHOS1; Site_l: Bst I; Constructed at The
/note="Vector: pHOS1; Site_l: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol
        whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and
Sequencing: A Practical Approach,
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ENTFUZ2TF Entamoeba histolytica
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Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences
HM1:IMSS sheared DNA library
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Entamoeba histolytica
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjloftus@tigr.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2000)
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/note="Vector: pHOS1; Site_1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytic
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Loftus, B., Van Aken, S. and Fraser, C. Determination of clone end sequences HM1: IMSS sheared DNA library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Brendan J Loftus
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                                                                                                                                                                                                                                                                                                                     /clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_1: Bst I; Constructed at Th
/note: The for Genomic Research (TIGR); Rockville, MD.
Genomic DNA isolated from broth cultures of E. histoly
using a method described by Clark and Dlamond (Clark,
using a method described by Clark and Dlamond (Clark,
                                                                                                                      whole genome shotun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and Barell, Oxford University Press, 1999)."

236 c 43 g 371 t
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/strain="HM1:IMSS"
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Score 74.8; DB 12;
Pred. No. 5.7e-05;
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SP_1031_A2_E05_SP6E Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus penomic clone Plate=1031 Col=10 Row=I, DNA sequence.

AZ196050

AZ196050.1 GI:8389873

GSS.
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                                                                                                                                                                                                                                                                                                                                                                          Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
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                                                                                                                                            Division of Biology 156-29
California Institute of Technology
Pasadena California 91125, USA
                                                                                                                                                                                                                                                                                                                                                                                                                         Strongylocentrotus purpuratus.
                                             Seq primer: SP6
Class: BAC ends
                                                                            Email: acameron@caltech.edu
Plate: 1031 row: I column
                                                                                                        Tel: (626) 395-8421
Fax: (626) 793-3047
                                                                                                                                                                                           Contact: Cameron, RA, Davidson, EH,
                                                                                                                                                                                                                                            additional resources
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quality sequence stop: 726.
Location/Qualifiers
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AZ550256
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ENTEV58TR Entamoeba histolytica
                                                                Email: bjloftus@tigr.org
Clones are derived from t
                                                                                                                                                                                            Loftus, B., Van Aken, S. and Fraser, C. Determination of clone end sequences HM1: IMSS sheared DNA library
High quality sequence start: High quality sequence stop:
                           Seq primer: M13-Reverse
Class: shotgun
                                                                                                                                                                  Contact: Brendan J Loftus
                                                                                                                                                                              Unpublished (2000)
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Best Local :
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2334 gggcaatgataaattagcatttgcagatgcaaat 2367
                                                                                                                                                                                                                                                                                                                                                                                                          1974 gggtaaacgtactgaaactatccagtatcgtgattatgaattaagaaaagttgggtatgg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1914 tcgtaaggttgctcgaggtgatatctaccatgaagttgtgaagcgtcaagaaaccaaggt
                                                                                                                                                                                   883 TATTCATTTGTTTGCATTATTACTAACTGTTCATGCCGAAGAAGATTCCTTTGACTTAGA 824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           823 TGAAAATGTAGAAATGGAACATGAATACCAGTTAGAAGACAATGAATTAGAAGAAGATGA
                                                                                                                                                                                                                                                                                                                                                                                       c9at99t9ct9ct9gtgac9accgctt9tttg9t99taaa9gcaacgatcgactttctgg
                                                                                tggtaatgatgtctatatctttcggaaaggtgatggtaatgatactttgtacgatggcac
                                                                                                                                    agatgaaggcgatgatttactcgatggcggttctggtgatgatgtattaaatggtggtgc
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Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
a 260 c 46 g 396 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib-"Entamoeba histolytica Sheared DNA"
/note-"Vector: pHOS1; Site_l: BSt I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 method for isolate identification. Exp. Parasitol
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Pred. No. 0.00012;
0; Mismatches 378;
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Matches 305;
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aggttgctcgaggtgatatctaccatgaagttgtgaagcgtcaagaaaccaaggtgggta 1978
                                                                       ACGACGATGATGATGAATTTGAATTAGAAGACGACGAAGAAGATGATGATGAAGAAGAAG
                                                                                                                                                                                         tgaatattgatggtggagatggacacgatcgtgtcttctatagtaaagacggaggatttg 1858
                                                                                                                                                                                                                                                      TTGCTTTATTCTTAACTGTTCATGCCGAAGAAGAGTTTGAACTCGATGATGTTTTGAAA 148
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                                                                                                             GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: bjloftus@tigr.org
Clones are derived from 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Brendan J Loftus
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Loftus, B., Wang, Z., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Ent
HM1:HMSS sheared DNA library (2001)
Unpublished (2001)
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/note="Vector: pHOS1; Site_1: Bst I; Constructed at The
/note="Vector: pHOS1; Site_1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
dsing a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. '(193) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + 1 method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole decome shefter in equations.
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63 c 280 g 218 t
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Entamoeba histolytica
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Pred. No. 0.0002;
0; Mismatches 388;
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                       Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a scale clone-end sequencing project of the Tetraodon nigrovirid genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSS; genome survey sequence
Tetraodon nigroviridis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Weissenbach, J_{\cdot} . Charaterization and repeat analysis of the compact Charater pufferfish Tetraodon nigroviridis .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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AL166032.1 GI:7803770
                                                                                                                                                                                                                     Genoscope
                                                                                                                                                                                                                                                                                 Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                            Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                               Tetraodon nigroviridis DNA sequence
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Location/Qualifiers
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Billault,A., Quetier,F., Saurin,W., Bernot
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                                                                                                                                                                                                                                                                                                                      9712 Medical Center Dr., Rockville, Tel: 301 838 0208 Fax: 301 838 3543
                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Entamoebidae; Entamoeba.

1 (bases 1 to 795)

Loftus,B., Van Aken,S. and Fraser,C.
Determination of clone end sequences
HM1:IMSS sheared DNA library
Unpublished (2000)
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The Institute for Genomic Researc
                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Brendan J Loftus
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                                                                                                                                                                                                                                                                 Seq primer: M13-Forward
                                                                                                                                                                                                                                                                                    DNA library
                                                                                                                                                                                                                                                                                                                   Email: bjloftus@tigr.org
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/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_l: Bst I; Constructed at The
/note="Vector: pHOS1; Site_l: Bst I; Constructed at The
/notitute for Genomic Research (TIGR); Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytic
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. parasitol.
77:450.). The DNA was mechanically sheared to give a
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197 c 95 g 117
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/db_xref="taxon:99883"
/clone="194601"
/clone_lib="G"
                                                                                                                                   /db_xref="taxon:5759"
                                                                                                                                                  /organism="Entamoeba histolytica"
/strain="HM1:IMSS"
                                                                                                                                                                                               Location/Qualifiers
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Pred. No. 0.00031;
3; Mismatches 83;
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                                                                                              AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gctggtaatgatgtctatatctttcggaaaggtgatggtaatgatactttgtacgatggc
                 Eukaryota; Entamoebidae; Entamoeba.

1 (bases 1 to 823)
Loftus B., Van Aken,S. and Fraser,C.
Determination of clone end sequences 1
HM1: IMSS sheared DNA library
Unpublished (2000)
Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                 AAACAAAATGTCAAAAAAATCCAAACTATTAAAAAATTAGATAACATTAGATTACCAAGA
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AZ676218
AZ676218.1 GI:11813364
                                                                                                                                                                                                                                                                 AZ676218 823 bp ENTKE36TR Entamoeba histolytica
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Department of Eukaryotic Genomics
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                                        acgggcaatgataaattagcatttgcagatgcaaatatatctgatattatgattgaacgt 2391
                                                                                                                                                                                                                                                                          GATGACGATGATGACGATGATGACGATGATGACGATGATGACGATGATGATGAC 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gtgggtaaacgtactgaaactatccagtatcgtgattatgaattaagaaaagttgggtat 2031
                                                                                        gctggtaatgatgtctatatctttcggaaaggtgatggtaatgatactttgtacgatggc 2333
                                                                                                                                                                                 GATGATGATGACGATGATGACGATGATGATGATGATGATGATGATGACGATGACGATGAC 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Institute for Genomic Research
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Similarity 44.8%;
69; Conservative
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/note="Vector: pHOS1; Site_l: BSt I; Constructed at The
/note="Vector: pHOS1; Site_l: BSt I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.) The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
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Pred. No. 0.00045;
0; Mismatches 331;
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Fax: 301 838 3543
Email: bjloftus@tigr.org
Clones are derived from t
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville
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/clone="vector: pHOS1; Site_1: Bst I; Constructed at The
/note="vector: pHOS1; Site_1: Bst I; Constructed at The
/note:-pHOS1; Site_1: 
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Sequencing: A Practical Approach, eds. M. Vaudin
Barell, Oxford University Press, 1999)."
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/strain="HM1:IMSS"
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Pred. No. 0.00045;
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Seq primer: M13-Reverse
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quality sequence stop: 677
Location/Qualifiers
/Clone_lib "Entamoeba histolytica Sheared DNA"
/clone_lib "Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_1: Bst I; Constructed at The
/note="Vector: pHOS1; Site_1: Bst I; Constructed at The
/nstitute for Genomic Research (TIGR), Rockville, MD.
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
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/strain="HM1:IMSS"
/db_xref="taxon:5759"
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BASE COUNT
ORIGIN
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Best Local Similarity 45.0%;
Matches 263; Conservative
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                                2272 gctggtaatgatgtctatatctttcggaaaggtgatggtaatga 2315
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Pred. No. 0.00046;
0; Mismatches 321; Indels 0
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Search completed: September 15, Job time: 41125 sec

2002, 09:51:07

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sequence sequence

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Sequence

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Total number of hits satisfying chosen parameters:
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Listing first 45 summaries
   Issued_Patents_NA:*

| (ggn2_6/ptodatta/2/ina/5A_COMB.seq:*
| (ggn2_6/ptodatta/2/ina/5B_COMB.seq:*
| (ggn2_6/ptodatta/2/ina/6A_COMB.seq:*
| (ggn2_6/ptodatta/2/ina/6B_COMB.seq:*
| (ggn2_6/ptodatta/2/ina/backfiles1.seq:*
| (ggn2_6/ptodatta/2/ina/backfiles1.seq:*
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US-08-95-4-418-1
US-07-960-932-1
US-07-960-932-1
US-08-45-970A-1
US-08-878-748-5
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US-07-960-932-9
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US-07-960-932-10
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                                                                                   TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
OCATION: 1.3294
US-07-777-715-6
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US-07-777-715-6
; Sequence 6, Application
; Patent No. 5273889
 Query Match
Best Local Similarity
Matches 1544; Conserv
                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: RODINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 29310-2001320
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-327-7250
                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Rela
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 19911016
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ADDRESSEE: Morrison & Foerster
STREET: 545 Middlefield Road, &
CITY: Menio Park
STATE: California
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APPLICANT: Hughes, Huw P.A.
TITLE OF INVENTION: CYTOKINE-LEUKOTOXIN GENE FUSIONS
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 9
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TYPE: N
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US-08-488-706-2
US-08-772-270A-9
US-08-488-706-3
PCT-US93-10500-1
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PCT-US95-08554-1

US-08-694-865-15

US-09-124-491-15

US-08-387-156-9

US-08-694-865-9

US-08-694-865-9

US-09-124-491-9
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 Score 815.6; DB 1;
Pred. No. 1.6e-177;
0; Mismatches 964;
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                                Length 3311;
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Score

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Gaps

9;

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Minimum

Maximum

DВ

Database

Title: Perfect score:

Sequence:

Scoring table:

Run

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US-08-170-126-1
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Patent No. 5594107
GENERAL INFORMATION:
                                                             TELEFAX: (415) 327-323 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
   TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: 1400
                                                                                   REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 900
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8899
TELEPAX: (415) 327-3231
                                                                                                                                                                             APPLICATION NUMBER: PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                     ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: CAMPOS, MANUEL
APPLICANT: HUGHES, HUW P.A.
TITLE OF INVENTION: CYTOKINE-CYTOTOXIN GENE
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3030
                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
                                                                                                                                                                                                                                                                  COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
  MOLECULE TYPE:
                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/170,126 FILING DATE: 20-DEC-1993
                                                                                                                                                                                                                                                                                                          COMPUTER:
                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                      STREET: 635 BRYAN CITY: PALO ALTO STATE: CALIFORNIA
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Best Local Similarity
Matches 1544; Conserva
CCAATATGATACTGAACAAGGTAATGGTTTACAGGATTTAGTCAAAGCGGCCGAAGAGTT
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                     aactatccagtatcgtgattatgaattaagaaaagttgggtatggttatcagtctaccga
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APPLICANT: POTTER, A
APPLICANT: CAMPOS, M
APPLICANT: HUGHES, H
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
                                                                                                                                                                                                                                                                      ZIP: 94301
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                      STATE: C
                                                                                                                                           APPLICATION NUMBER: FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: STREET: 6
                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
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CYTOKINE-CYTOTOXIN GENE FUSIONS AND
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; LOCATION:
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TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3311 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 29.3
Best Local Similarity 60.1
Matches 1544; Conservative
                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
810 tgctggtctatcaactactggtgctgttgctgctttaatttacttcatcgattatgttggc
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                                                                                                                                                                                                                                                                                                                                                                                                                                    333 aaatattgatcgtaaattaggtaaagcaagtaatgtattatcaacattaagctctttttt 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               711 CACGATTCAAACCGCTATTGGCTTAACTGAGCGTGGCATTGTGTTATCCGCTCCACAAAT
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                                                       tcaagttattggtaatgtaacaaaagcaatttcttcatatgttttagcacaacgtgttgc
                                                                                             ACTTGCAGATAAAAATGCTTCAACAGCTAAAAAAGTGGGTGCGGGTTTTGAATTGGCAAA
                                                                                                            tttagcggataaaaatgcatcgactggcaaaaaagttgctgcaggtttttgaattaagcaa
                                                                                                                                                                                                                                                        TTCAGTAAAAACACTTGACGAATTTGGTGAGCAAATTAGTCAATTTGGTTCAAAACTACA
                                                                                                                                                                                                                                                                      AGGCTCAGTATTGGCTGGAATGGATTTAGATGAGGCCTTACAGAA---TAACAGCAACCA
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Pred. No. 1.6e-177;
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	S	CT + CAT + C	χ Σ	Q
	1868	tggtggagatggacacgatcgtgtcttctatagtaaagacggagatttggtaatattac tggtggagattgacacgatcgtgtcttctatagtaaagacggagatttggtaatattac 	2319	Db Qy
	33	GCCAAACTTGGTGAAGGTGATGACAACGTATTTGTTGGTTCTGGTACGACGGAAATTGA	25	Db
	1808	gctggcaatgacgatatctttgttggtcaaggtaaaatgaatattga	1762	Qy
	2258		1	Db
	1761	glagccgagacagaaggcacagacgagattggtctaatagtaaatgcaaa	1710	Qy
	2198	CTGGAAAATTACAGATGGTGCAGCAAGTTCTACCTTTGATTTAACTAAC	2139	Db
	1709	tggcaagttacagatggagaggctagttctaaattagatttctctaaagttattcagcg	1650	Qy
	2138	ACGCGTACAAACAGGTAAATATGAATATTACCAAGCTCAATATTAACCGTGTAGATAG	2079	Дb
	1649	cytttaactaatyytaaatactcttatattaataayttaaaattcygacytytaaaa	1590	Qy
	2078	TCTTATTCAGAACGCCATTATTGACGCCGGGAACAGAGCATCGTGA	2019	Db
	1589	aaaacgcaagcgttgcatttcacttcgcctttgttaacagcaggaactgaatcacgtga	G	Оу
	2018	TAAATTAGTACAGTTGGATTCGGCAAACGGTATTATTGATGTGAGTAATTCGGGTAAAGC	1959	Дb
	1529	tccaatattactttggatgctaaaactggtatcatagacattagtaattcaaa	1470	Qy
	1958	AAAGC	1899	Db
	1469	taagagcggaaaagcttatgcagatgcttttgaagatggcaagaaagttgaagctg	1410	Qy
	1898	TCAGCAGCAATGGGATAACAACATTGGTGATTTAGCTGGTATTAGCCGTTTAGGTGAAAA	1839	Db
	1409	aacaacgttgggataataatattggtgagttagcaggtattaccaaattgggtgaacg	1350	Qy
	1838	CTGAACTTAAACAAAGAGTTACAGGCAGAACGTGTCATCGCTATTAC	1779	Db
	1349	aaatttttgtctgagctaaataaagagttggaagctgaacgtgttattgcaatcac	1290	Qy
	1778	CGGTAAGAACTACTTTGAAAATGGTTACGATGCCCGTTATCTTGCGAATTTACAAGATAA	1719	дb
	1289	ggtcagaactattttgataaaggctatgattctcgttatgctgcttatttagctaat		Qy
•	1718	AAAATTCATAACAAAATTGTAGAATGGGAAAAAAATAATCA	1659	Db
	1229	tttgaaagtgttgctaaccgtttacaaggtaaaattttagagtgggaaaagcaaa	1170	Qy
	1658		S	Db
	1169	agttgcaggtgttacaggattgatctctggaattttagaagcgtctaaacaggo	1110	Qy
	1598	TATTGCTGGTGGTGTCTGCTGCTGCTGCAGCCGGCTTATTGCTTCACCGATTGCCTT	1539	Db
	1109	ttotgotggtgtttoogotgctgctgtaggatotgctgttggtgcaccgattgcact	0	Qy
	1538	ACAGGGACTATTGATGCATCGGTTACTGCAATTAATACCGCATTGGCCGC	1479	Db
	1049	cagcgtggtgtgggtactattgaagcttcattaactacaattagtacggcattaggtgc	990	Qy
	1478	AGTTATGCCGAACGCTTTAAAAAATTAGGCTATGACGGAGATAATTTATTAGCAGAATA	1419	Db
	989	ttgcaaaacaattccgaaaatttggctatgatggggatcatttattggctgaata	930	Qy
			1359	Db
	29	attagtcctttggcatttatgaatgcagcagataaattcaatcatgctaatgctcttga	7	Qy
	1358	AGCAGGTTTATCTTCAACTGGGCCTGTGGCTGCTTTAATTGCTTCTACTGTTTCTCTTGC	1299	Db

ATTORNEY/AGENT INFORMATION:

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                                                                                                                                                                                                                                                                                                                         APPLICANT: POTTER, ANDREW A.
APPLICANT: REDMOND, MARK J.
APPLICANT: HUGHES, HUW P.A.
TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN
TITLE OF INVENTION: CHIMERAS
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                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSE: ROBERTA L. ROBINS
STREET: 635 BRYANT STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2970
                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                STREET: 635 BRYAN'
CITY: PALO ALTO
STATE: CALIFORNIA
FILING DATE: 1 CLASSIFICATION:
                  APPLICATION NUMBER: US/07/960,932 FILING DATE: 19921014
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Best Local
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LO NO:

ACTERISTICS:

LYPE: NUCLEIC ACID

STRANDEDNESS:

TOPOLOGY:

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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
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                                          atgcatcgactggcaaaaaagttgctgcaggttttgaattaagcaatcaagttattggta
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Pred. No. 2.9e-177;
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RESULT 5 US-07-908-253-1

Sequence 1, Application Patent No. 5534256

US/07908253

GENERAL INFORMATION:

APPLICANT: POTTER, ANDREW A.
APPLICANT: HARLAND, RICHARD J.
TITLE OF INVENTION: HAEMODHILUS SOMNUS OUTER MEMBRANE
TITLE OF INVENTION: PROTEIN EXTRACT ENRICHED WITH IRON-REGULATED

PROTEINS

COUNTRY: UNITED STATES OF AMERICA ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-OOS/MS-DOS
SOFTWARE: Patentin Release #1.0, v

Version

# . 25 AMERICA

NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBERTA L. ROBINS
STREET: 635 BRYANT STREET
CITY: PALO ALTO
STATE: CALIFORNIA

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US-07-908-253-1
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Best Local Similarity
Matches 1538; Conserv
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INFORMATION FOR SEQ ID NO: 17
SEQUENCE CHARACTERISTICS:
LENGTH: 2794 base pairs
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REGISTRATION NUMBER: 3,208
REFERENCE/DOCKET NUMBER: 9000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEPAX: (415) 327-3231
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APPLICATION NUMBER: US
FILING DATE: 19920702
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CLASSIFICATION:
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atgcatcgactggcaaaaaagttgctgcaggtttttgaattaagcaatcaagttattggta
                                  TAGATGTTATCTCAGGGCTATTATCGGGCGCAACAGCTGCACTTGTACTTGCAGATAAAA
                                                                                                                  AAGCTGGCTTGGAGCTAACAAATTCATTAATTGAAAATATTGCTAATTCAGTAAAAACAC
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Pred. No. 2.9e-177;
0; Mismatches 956;
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Gaps

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ARGCTTAACAGCTAAAAAGTGGGTGGGTTTTGAATTGGCAAACCAAGTTGTGGGTAAAAAGTGGTGGGGTTTTGAATTGGCAAACCAAGTTGTTGGGTAATAGCAAGTTGTTGGGTAAAAAAGTTGTGGGAAAAAAAA	Qy	Db	Qy	Db 4	Q	Db 43		pb Qy	Db	Qy	DЬ	Qy	Дb	Qy	рь	Qy	B 2	Q	Db X	0 V	pb Qy	)	Db 49	) <u>(</u>	J (2	, p	, oy	Db	ОУ	Db	Qy	Db	ο <sub>ν</sub>	Db
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US-08-455-970A-1
                                                                                                                                                                                                                                              Sequence 1, Application US/08455970A Patent No. 5708155
GENERAL INFORMATION:
                                                                                                                               APPLICANT: POTTER, ANDREW A. APPLICANT: REDMOND, MARK J. APPLICANT: HUGHES, HUW P.A. TITLE OF INVENTION: ENHANCED: TITLE OF INVENTION: CHIMERAS NUMBER OF SEQUENCES: 15
                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & RC
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                 CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF
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; LOCATION:
US-08-455-970A-1
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Best Local Similarity
Matches 1538; Conserv
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TELEPHONE: (415) 327-3400
TELEPAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/
FILING DATE: 31-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 14-OCT-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
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FEATURE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53 caaagtctggattaaaaaatctttacttggctattcccaaagat-----tatgatccgc 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE:
COMPUTER: II
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tctctaatataggaaacaagttgcaaaacttaaat---ttttctaaaacaaatcttggtt 643
                                                                                                                                                         CTGGAATGGATTTAGATGAGGCCTTACAGAA---TAACAGCAACCAACATGCTCTTGCTA
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                                                                                 ttgaagcattttcttcacagttagcaaagttaggttctactatatcgcaggctaaaggct 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAAGAGAAGAACGCAATAATTGCAACAGCTCAAACCAGTTTAGGCACGATTCAAACCG
                                             TTGACGAATTTGGTGAGCAAATTAGTCAATTTGGTTCAAAACTACAAAATATCAAAGGCT
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Pred. No. 2.9e-177;
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RESULT 7
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US-08-387-156-5
Sequence 5, Application US/08387156
Sequence 5, Application US/08387156
Fatent No. 5723129
GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: REDMOND, MARK J.
APPLICANT: HUGHES, HUW P.A.
TITLE OF INVENTION: GORH-LEUKOTOXIN CHIMERAS
NUMBER OF SEQUENCES: 28

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Best Local Similarity 60.2%;
Matches 1538; Conservative
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APPLICATION NUMBER: US 07/960,932

FILING DATE: 14-OCT-1992

PRIOR APPLICATION DATA:

APPLICATION UMBER: US 07/779,171

FILING DATE: 16-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: ROBINS, ROBERTA L.

NAME: ROBINS, ROBERTA L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FLOPPY disk
COMPUTER: PM PC COMPATIBLE
COMPUTER: PATENT PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: US/08/387,156
FILING DATE: 10-FEB-1995
CLASSIFICATION: 424
CLASSIFICATION: 424
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REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
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1183 1156	4 ttacaggattgatctctggaattttagaagcgtctaaacaggcaatgtttgaaagtgtttg 	112, 109	Qy Db	
1123 1096	4 tttccgctgctgctgtaggatctgctgttggtgcaccgattgcactattagttgcaggtg	106,	Qy Db	
1063	4 gtactattgaagcttcattaactacaattagtacggcattaggtgcagtttctgctggtg	100 <b>4</b> 977	Qy Db	
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               gttatatcacttccgatcaaattgataaaatttt
                                                         TGCCTAATTATAAAGCAACTAAAGATGAGAAAATCGAAGAAATCATCGGTCAAAATGGCG
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AGCGGATCACCTCAAAGCAAGTTGATGATCTTAT
                                                                                                                GCAAAAAAGAGAAAGTGACCATTCAAAACTGGTTCCGAGAGGCTGATTTTGCTAAAGAAG
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RESULT 8
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REFERENCE/DOCKET NUMBER: 9001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)327-3400
TELEPHONE: (415)327-3231
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2794 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/08694865 Patent No. 5837268 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                Matches 1538;
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: POTTER, ANDRAPPLICANT: MANNS, JOHN TITLE OF INVENTION: GRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION: NAME: MCCRACKEN, THOMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
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                                                                               aaaaacattctaccaataagttagccaaaagggttagacagtgtagaaaatattgatcgta
                                                                                                                                         ttctctctctcacacaaactggtattgctatttctgcaacaaaattagaaaagttcttac
                                                                                                                                                                                                       tagcagaagagcctaatcacactgaaacagcaaaaaaatctgttgacacagtaaatcagt 226
                                                                                                                                                                                                                                                                    aaaaaggtgggactttaaatgattttattaaagctgctgatgaattaggtattgctcgtt 166
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ATGCAAATAAAGCCAAAACTGTATTATCTGGCATTCAATCTATTTTAGGCTCAGTATTGG
                  aattaggtaaagcaagtaatgtattatcaacattaagctctttttttgggcactgcattag
                                                                                                                        CTATTGGCTTAACTGAGCGTGGCATTGTGTTATCCGCTCCACAAATTGATAAATTGCTAC
                                                                                                                                                                                       AAAGAGAAGAACGCAATAATATTGCAACAGCTCAAACCAGTTTAGGCACGATTCAAACCG
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Pred. No. 2.9e-177;
0; Mismatches 956;
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1543	tggatgctaaaactggtatcatagacattagtaattcaaatgggaaaaaaaa	1484	Qγ
1456	AGCCTATGTGGATGCGTTTGAAGAAGGCAAACACATTAAAGCCGATAAATTAGTACAGT	1397	밁
	agcttatgcagatgcttttgaagatggcaagaaagttgaagctggttccaatattactt	1424	Qy
1396	STEGTA	1337	В
1423	aataatattggtgagttagcaggtattaccaaattgggtgaacgcattaagagcgga	1364	Qy
1336		1277	DЬ
1363	gagctaaataaagagttggaagctgaacgtgttattgcaatcacccaacaacgttgg	1304	Qy
1276	TTGAAAATGGTTACGATGCCCGTTATCTTGCGAATTTACAAGATAATATGAAATTCTTAC	1217	Ъ
1303	tyataaayyotatyattotogttatyotyottatttagotaataaottaaaattttt	1244	δ
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916	ATTTGCCGGTATTGCCGATAAATTTAATCATGCAAAAAGTTTAGAGAGTTATGCCGAA	857	В
943	tgaatgcagcagataaattcaatcatgctaatgctcttgatgagtttgc	884	Qy
856	CTGGGCCTGTGGCTTTAATTGCTTCTACTGTTTCTCTTGCGATTAGCCCA	797	Дb
883	tactggtgctgttgctttaattacttcatcgattatgttggcaattagtcctttg	824	Qy
796	ATATTACCAAAGCCGTTTCTTCTTACATTTTAGCCCAACGTGTTGCAGCAGGTTTATCTT	737	В
823	taacaaaagcaatttottoatatgttttagcacaacgtgttgctgctggtctatca	764	Qy
763 736	atgcatcgactggcaaaaaagttgctgcaggttttgaattaagcaatcaagttattggta	704 677	Db 40
7	gatgttatctcagggctattatcgggcgcaacagctgcacttgtacttgcagat <i>i</i>		DЬ
703	tggaaataattactggtttgctatcaggcatttctgcaggctttgctttagcgggataaaa	644	Qy
616	AGGGACTTTAGGAGACAAACTCAAAAATATCGGTGGACTTGATAAAGG	557	Db
643	taatataggaaacaaattgcaaaacttttctaaaacaaatcttgg	587	Qy
556	TCAAAACTACAAA	497	В
586	gaagcattttcttcacagttagcaaagttaggttctactatatcgcaggctaaaggc	527	Qy
9			Db .
Ň	gctaqtattqacttqattaatqaqataattqqtaatctatct		Qy
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466	grafagaacrtgartctttaatcaaaaaaggtgatgctgcacctgatgctttggcta	407	Qy

2243 gttctggtgatgatgtattaaatggtggtgctggtaatgatgtctatatctttcggaaag	
2243 gttctggtgatgatgtattaaatggtggtgctggtaatgatgtctatatctttcggilling canal cana	
2243 gttctggtgatgatgtattaaatggtggtgctggtaatgatgtctatatctttcggilling colored co	
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2243 gttctggtgatgatgtattaaatggtggtgctggtaatgatgtctatatctttcggaaag	
2171 TIGGTGGTAAAGGCGATGATATTCTC	
TTAACGGTGGTGATGGTGTCGATACTATTGACGGTAACGACGGCAATGACCGCTTAT	
2123 tattccatagtggtgaaggtgatgatttactcgatggtggtggtggtggtgacgaccgcttgt	
AAGAAATTATCGGTACATCACATAACGATATCTTTAAAGGTAGTAGTTCAATGATG	
gaagaagtaattggttctcaatttaatgatgtattcaaaggttctaaattcaacga	
Oy 2003 gtgattatgaattaagaaaagttgggtatggttatcagtctaccgataatttgaaatcag 2	
1934 ACGAAGTGACCTTCAACCCATACCGCATTAGTGGGCAACCGTGAAGAAAAAATAGAATATC	
tgaagttgtgaagcgtcaagaaaccaaggtgggtaaacgtactgaaactatccagtat	
CGTAGAAACCGGTA	
1883 grącaacagaagcaggcagrtatacagrtaatcgraaggrtgctcgaggrgatatctac	
Db 1817 ACGACCGAGTTCACTATAGCCGTGGAAACTATGGTGCTTTAACTATTGATGCAACCA 1	
1757 AAGGTGATGACAACGTATTTGTTGGTTCTGGTACGACGGAAATTGATGGCGGTGAAGGTT	
1763 ctggcaatgacgatatctttgttggtcaaggtaaaatgaatattgatggtggagatggac 	
GACAATGCTGGAAATGTAACTAAAACCAAAGAAACAAAAATTATTGCCAAACTTGGT	
gattggtct 	
GGTGCAGCAAGTTCTACCTTTGATTTAACTAACGTTGTTCAGCGTATT	
tggagaggctagttctaaattagatttctctaaagttattcagcgtgtagccgaga	
Db 1577 GTAAATATGAATATTACCAAGCTCAATATTAACCGTGTAGATAGCTGGAAAATTACAG 1	
taaatactcttatattaataagttaaaattcggacgtgtaaaaaactggcaagttac	
Oy 1544 tgcattcacttcgcctttgttaacagcaggaactgaatcacgtgaacgtttaactaatg l	
57 TGGATTCGGCAAACGGTATTATTGATGTGAGTAATTCGGGTAAAGCGAAAACTCAGCA	

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US-08-878-748-5
US-08-878-748-5
; Sequence 5, Application US/08878748
• patent No. 5969126
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US-08-878-748-5
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Best Local S
Matches 1538
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FILING DATE: 10-FEB-195
APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-OCT-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: REDMOND, MARK J.
APPLICANT: HUGHES, HUW P.A.
TITLE OF INVENTION: GNRH-LE
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/779,171 FILING DATE: 16-OCT-1991 ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: ROBINS, ROBERTA L. REGISTRATION NUMBER: 33,208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 19-JUN
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CITY: PALO ALTO
                                                                                                                                                                                                    Local Similarity
les 1538; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
                 AAAGAGAAGAACGCAATAATATTGCAACAGCTCAAACCAGTTTAGGCACGATTCAAACCG
                                                                                           aaaaaggtgggactttaaatgattttattaaagctgctgatgaattaggtattgctcgtt 166
                                                                                                                                       caaagtctggattaaaaaatctttacttggctattcccaaagat-----tatgatccgc 106
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                                           tagcagaagagcctaatcacactgaaacagcaaaaaaatctgttgacacagtaaatcagt
                                                                           AACAAGGTAATGGTTTACAGGATTTAGTCAAAGCGGCCGAAGAGTTGGGGATTGAGGTAC
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(415) 327-3231
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US-08-535-837-1
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US-08-535-837-1
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                                                                                                                             Query Match
Best Local Similarity
Matches 1538; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application Patent No. 5985289
                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION UMBER: US/08/535, FILING DATE: 27-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-3400
TELEFAX: (415) 327-3231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (415) 327-32
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: POTTEK, AND J.

APPLICANT: HARLAND, RICHARD J.

APPLICANT: HARLAND, RICHARD J.

TITLE OF INVENTION: HAEMOPHILUS SOMNUS OUTER J.

TITLE OF INVENTION: PROTEIN EXTRACT ENRICHED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBERTA L. ROBINS
STREET: 285 HAMILTON AVENUE,
                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 2794 base pairs
TYPE: nucleic acid
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CITY: PALO ALTO
STATE: CALIFORNIA
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                 caaagtctggattaaaaaatctttacttggctattcccaaagat-----tatgatccgc 106
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                                                                                                                           Score 814.4; DB 2;
Pred. No. 2.9e-177;
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1216	CAAATAAAATTCATAACAAAATTGTAGAATGGGAAAAAATAATCACGGTAAGAACTAC	1157	B
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Ū	GACTATTGATGCATCGGTTACTGCAATTAATACCGCATTGGCCGCTATTGCTGGTGGT	977	Db
6	actattgaagcttcattaactacaattagtacggcattaggtgcagtttctg 	1004	Qy
976	GCTTTAAAAAATTAGGCTATGACGGAGATAATTTATTAGCAGAATATCAGCGGGG	917	DЪ
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943 916	cagataaattcaatcatgctaatgctcttgatgagtttgo 	884 857	Qy Дъ
856	AACTGGGCCTGTGGCTTTAATTGCTTCTACTGTTTCTCTTGCGATTAGCCCATTA	797	Db
	ctactggtgctgttgctgctttaattacttcatcgattatgttggcaattagtcctttgg	824	Qy
796	TTACCAAAGCCGTTTCTTCTTACATTTTAGCCCAA	737	DЬ
823	tgtaacaaaagcaatttcttcatatgttttagcacaacgtgttgctgctggtctatc	764	Qy
		677	Db
763	tgcatcgactggcaaaaagttgctgcaggttttgaattaagcaatcaagttattggt	704	Qy
7	TTATCTCAGGGCTATTATCGGGCGCAACAGCTGCACTTGTA	617	Db 4
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556	TGACGAATTTGGTGAGCAAATTAGTCAATTTGGTTCAAAACTACAAAATATCAAAGGC	497	Db
586	ttcacagtt	527	Qy
9	GCTTGGAGCTAACAATTCATTAATTGAAAATATTGCTAATTCAGTAAAAACA	437	Db
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466 436	<pre>cgggttatagaacttgattctttaatcaaaaaaggtgatgctgcacctgatgctttggctt</pre>	4 07 380	Оγ
7	TGCAAATAAAGCCAAAACTGTATTATCTGGCATTCAATCTATTTTAGGCTCAGTATTG	320	Db
0	aattaggtaaagcaagtaatgtattatcaacattaagctctttttttgggcactgcattag	347	Qy
319	AAACTAAAGCAGGCCAAGCATTAGGTTCTGCCGAAAGCATTGT	269	Db
346	aaacattotaocaataagttagocaaagggttagacagtgtagaaaatattgatcgt	287	Ωу
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226 208	tagcagaagagcctaatcacactgaaacagcaaaaaaaatctgttgacacagtaaatcagt 	167 149	P 04

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tcggaaag 2302          CCGTAAAG 2290	gttctggtgatgatgtattaaatggtggtgctggtaatgatgtctatatcttt	22 <b>4</b> 3 2231	Qy Db	
cgatggcg 2242           CGATGGCG 2230	ttggtggtaaaggcaacgatcgactttctggagatgaaggcgatgattactc	2183 2171	Qy Db	
ccgcttgt 2182	tattccatagtggtgaaggtgatgatttactcgatggtggtggtggtggtggtgacgar 	2123	Qy Db	
caacgaca 2122        CAATGATG 2110	tagaagaagtaattggttctcaatttaatgatgtattcaaaggttctaaattv	2063 2051	Qy Db	
gaaatcág 2062           GAAAGCTG 2050	gtgattatgaattaagaaaagttgggtatggttatcagtctaccgataattts	2003 1994	Qу	
ccagtatc 2002        AGAATATC 1993	atgaagttgtgaagcgtcaagaaaccaaggtgggtaaacgtactgaaactatc	1943 1934	Оy	
tatotacc 1942	gtgcaacagaagcaggcagttatacagttaatcgtaaggttgctcgaggtgail	1883 1874	Qy Db	
tggtacga 1882	acgatcgtgtcttctatagtaaagacggaggatttggtaatattactgtagat 	1823 1817	Оу	
gatgg       GAAGG	ctggcaatgacgatatctttgttggtcaaggtaaaatgaatattgatggtgga 	1763 1757	ДУ	
ACTTGGTG 1756	aaggcacagacgagattggtctaatagtaaatgcaaaa	1724 1697	ОУ	
cgagacag 1723     TATTGAAT 1696	atggagaggctagttctaaattagatttctctaaagttattcagcgtgtagcc 	1664 1637	Qy Db	
ycaagttacag 1663              JAAAATTACAG 1636	gtaaatactcttatattaataagttaaaattcggacgtgtaaaaaaactggcaa 	1604 1577	Db Oy	
aactaatg 1603 	tgcatttcacttcgcctttgttaacagcaggaactgaatcacgtgaacgttta 	1544 1517	Qу	
gcaagcgt 1543    TCAGCATA 1516	tggatgctaaaactggtatcatagacattagtaattcaaatgggaaaaaaacgcg 	1484 1457	Ду	
ratattactt 1483   1   TAGTACAGT 1456	aagcttatgcagatgcttttgaagatggcaagaagttgaagctggttccaat	1424 1397	Оу	
gagcggaa 1423          TAGTGGTA 1396	ataataatattggtgagttagcaggtattaccaaattgggtgaacgcattaag:	1364 1337	Qy Db	
acgttggg 1363         GCAATGGG 1336	ctgagctaaataaagagttggaagctgaacgtgttattgcaatcacccaacaa	130 <b>4</b> 1277	Qу	
 ATTCTTAC 1276		1217	Db	

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US-09-124-491-5
                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/694,865
FILING DATE: 09-40G-1996
APPLICATION NUMBER: US 08/387,156
FILING DATE: 10-FEB-1995
PRIOR APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-OCT-1992
PRIOR APPLICATION NUMBER: US 07/779,171
FILING DATE: 16-OCT-1991
ATPORNEY/AGENT INFORMATION:
NAME: MCCRACKEN, THOMAS P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 9001-0016.22
TELECOMMUNICATION: UFORMATION:
TELEPHONE: (415)327-3400
TELEPHONE: (415)327-3400
TELEPAX: (415)327-3231
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2794 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS LLP
STREET: 285 HAMILTON AVENUE, SUITE 200
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APPLICANT: MANNS, JOHN G.
TITLE OF INVENTION: GRH-LEUKOTOXIN CHIMERAS
NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2528 AGCGGATCACCTCAAAGCAAGTTGATGATCTTAT 2561
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                                                                 FEATURE:
                                                                                   MOLECULE TYPE:
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CITY: PALO ALTO
STATE: CA
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                                                                                                       TOPOLOGY:
                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: doub
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/124,491 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: UZIP: 94301
                                         NAME/KEY:
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 TTGAAGAAATTATCGGTACATCACATAACGATATCTTTAAAGGTAGTAAGTTCAATGATG
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/15
FILING DATE: 09-FEB-193
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 504,850
FILING DATE: 05-APR-1990
APPLICATION NUMBER: 335,018
FILING DATE: 07-APR-1989
SEQ ID NO:2:
LENGTH: 2794
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5476657-2
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APPLICANT: POTTER, ANDREW A.

TITLE OF INVENTION: PASTEURELLA HAEMOLYTICA

COMPOSITIONS AND USES THERROF

NUMBER OF SEQUENCES: 8
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Best Local Similarity 60.2%;
Matches 1538; Conservative
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                                                     aaagagaagaacgcaataatattgcaacagctcaaaccagtttaggcacgattcaaaccg
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Pred. No. 2.9e-17
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1336	tgaacttaaacaaagagttacaggcagaacgtgtcatcgctattactcagcagcaatg	1277	В
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US-07-960-932-9
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                                                                                                                                                                   Query Match
Best Local Similarity
Matches 1538; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 2817 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: POTTER, A
APPLICANT: REDMOND,
APPLICANT: HUGHES, I
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: ROBINS, ROBERTA L
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 900
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 19921014
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
 149
                           167
                                                                                                                                                                                                                                                     NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
CITY: PA
STATE: C.
COUNTRY:
                                                       89
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                                                      AACAAGGTAATGGTTTACAGGATTTAGTCAAAGCGGCCGAAGAGTTGGGGATTGAGGTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: ROBERTA L. ROBINS
635 BRYANT STREET
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HUGHES, HUW P.A.
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                                                        Query Match 29.3
Best Local Similarity 60.3
Matches 1538; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                  TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 2817 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,970A
FILING DATE: 31-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: HUGHES, HUW P.A.
TITLE OF INVENTION: ENHANCE
TITLE OF INVENTION: CHIMERA
                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
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LOCATION:
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STATE: CALIFORN
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                                                                                                                                                                                                                                    TYPE: nucleic acid
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(415) 327-3231
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Pred. No. 2.9e
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Query Match
Best Local Similarity
                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM_PC_COMPATIBLE
OPERATING SYSTEM: PC-DOS_MS-DOS
SOFTWARE: PATENTIAN
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/960,932
FILING DATE: 19921014
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 2838 base pairs
                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
RECISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 900
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MEDIUM TYPE: Floppy disk
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                                                                                                                FEATURE:
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CITY: PALO ALTO
STATE: CALIFORN:
                                                                                                                                              TOPOLOGY:
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635 BRYANT
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Score 814.4; DB 1;
Pred. No. 2.9e-177;
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TGTCTGCTGCAGCCGGCTCGGTTATTGCTTCACCGATTGCCTTATTAGTATCTGGGA 1096
             GCTTTAAAAAATTAGGCTATGACGGAGATAATTTATTAGCAGAATATCAGCGGGGAACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAGATGTTATCTCAGGGCTATTATCGGGCGCAACAGCTGCACTTGTACTTGCAGATAAAA
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                                                                                                                                                                                               CATTTGCCGGTATTGCCGATAAATTTAATCATGCAAAAAGTTTAGAGAGTTATGCCGAAC
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2182 2170	23 tattccatagtggtgaaggtgatgatttactcgatggtggtggtggtgacgaccgcttgt	Qy 21 Db 21	
2122 2110	63 tagaagaagtaattggttetcaatttaatgatgtattcaaaggttettaaattcaacgaca 	Qy 20 Db 20	п О
2062 2050	03 gtgattatgaattaagaaaagttgggtatggttatcagtctaccgataatttgaaatcag	9	пΩ
2002 1993	agc CAA	Qy 19 Db 19	по
1942 1933	83 gtgcaacagaagcaggcagttatacagttaatcgtaaggttgctcgaggtgatatctacc	ထ ထ	по
1882 1873	Jtac   	<b>ω ω</b>	пΩ
1822 1816	aaaatgaatattgatggtggagatggac 	Qy 17: Db 17:	п о
1762 1756	4 aaggcacagacgagattggtctaatagtaaatgcaaaa	7	U 0
1723 1696	4 atggagaggctagttctaaattagatttctctaaagttattcagcgtgtagccgagacag 	Qy 166 Db 163	ט ט
1663 1636	4 gtaaataststttattaataagttaaaattoggacgtgtaaaaaactggcaagttacag 	· = -	ם ס
1603 1576	4 tgcatttcacttcgcctttgttaacagcaggaactgaatcacgtgaacgtttaactaatg	15 5	gg Vg
1543 1516	4 tggatgctaaaactggtatcatagacattagtaattcaaatgggaaaaaaacgcaagcgt 	- н	d Vo
4 4	4 aagcttatgcagatgcttttgaagatggcaagaaagttgaagctggttccaatattactt	-	P 40
1423 1396	4 ataataatattggtgagttagcaggtattaccaaattgggtgaacgcattaagagcggaa 	у 136 b 133	Оу
iu iu	4 ctgagctaaataaagagttggaagctgaacgtgttattgcaatcacccaacaacgttggg :	y 130 b 127	Qу
1303 1276	gctaataacttaaaatttttgt                  CAAGATAATATGAAATTCTTAC		dd Yg
1243 1216	.acaaggtaaaattttagagtgggaaaagcaaaatggcggtcagaactatt 	118 115	da Yo
1183 1156	4 ttacaggattgatctctggaattttagaagcgtctaaacaggcaatgtttgaaagtgttg 1 	112	dd YQ

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2528 AGCGGATCACCTCAAAGCAAGTTGATGATCTTAT 2561
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Search completed: September 15, 2002, 11:17:13 Job time: 15360 sec

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## ALIGNMENTS

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Q1-MAR-2001
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                                                                                                                                            Bacteria; Proteobacteria; Mannheimia.
 MEDILINE-21101823; PubMed-11157953;
Davies R.L., Whittam T.S., Selander R.K.;
"Sequence Diversity and Molecular Evolution of
Gene in Bovine and Ovine Strains of Mannheimia
                                                                                                                          NCBI_TaxID=85401;
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16,
19,
                                                                                                                                                               gamma
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Last sequence up
Last annotation
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                                                                                                                                                                   subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                    927
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                                                                                                                                                                                                                                                                                                              AA
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                        the Leukotoxin
       (Pasteurella
                          (lktA)
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Best Local
Matches 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Bacteriol. 183:1394-1404(2001).

REMBL; AF314521; AAG40305.1; -.

InterPro; IPR001753; Enoyl_Co_hydrtse.

InterPro; IPR001343; Hemlysn_Ca_bind.

InterPro; IPR003355; RTX_N.

Pfam; PF00353; hemolysinCabind; 1.

Pfam; PF02382; RTX; 1.

PFANTS; PR00313; CABNDWGRPT.

PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.

PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     haemolytica.";
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                                                                                                                                                                                                                                                                                                                                                                                                                        471;
                                                                                                                                                                                                                                                                      OSTQTIEAFSSQLAKLGSTISQAKGFSNIGNKLQNLN-FSKTNLGLEIITGLLSGISAGF
                                                                                                                                                                                                                                                                                                                                                            ENLTKGFSNAKTVLSGIQSILGSVLAGMDLDEALQK-NSNELTLAKAGLELTNSLIENIA
                                                         AISPLAFMNAADKFNHANALDEFAKQFRKFGYDGDHLLAEYQRGVGTIEASLTTISTALG
                                                                                                                                                                                                                                                                                                                                               ENIDRKLGKASNVLSTLSSFLGTALAGIELDSLIKKGDAAPDALAKASIDLINEIIGNLS
IVNAKAGNDDIFVGQGKMNIDGGDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNRKVA
                                                                                                                     ERVQTGKYEYITKLNINRVDSWKITDGAASSTFDLTNVVQRIGIELDNAGNVTKTKETKI
                              SKFNDIFHSGEGDDLLDGGAGDDRLFGGKGNDRLSGDEGDDLLDGGSGDDVLNGGAGNDV
                                                                                                                                   ERLINGKYSYINKLKFGRVKNWQVTDGEASSKLDFSKVIQRV----
                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 49.9%; Pr 71; Conservative 182;
                                                                                                                                                                                                                                                                                                                                                                                                                               50.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 2358.5;
Pred. No. 4.1e
82; Mismatches
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4.1e-97;
hes 258;
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Best Local Similarity
Matches 471; Conserv
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01-MAR-2001
01-MAR-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                            J. Bacteriol. 183:1394-1404(2001).
EMBL; AF314522; AAG40306.1; -.
InterPro; IPR001753; Encyl_Coa_hyd
InterPro; IPR001343; Hemlysn_Ca_bi
InterPro; IPR003355; RTX_N.
                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00313; CABNDNGRPT.

PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1
SEQUENCE 953 AA; 102150 MW; D99C36DA595B1624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Davies R.L., Whittam T.S., Selande "Sequence Diversity and Molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9EV23
                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00353; hemolysinCabind; Pfam; PF02382; RTX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene in Bovine and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-PH290;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mannheimia glucosida.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                haemolytica.";
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SLIENIANSVKTLDAFGDQINQLGSKLQNVKGLSSLGDKLKGLSGFDKTSLGLDVVSGLL
                                                                                                                                     EIIGNLSQSTQTIEAFSSQLAKLGSTISQAKGFSNIGNKLQNLN-FSKTNLGLEIITGLL
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                                                                                                                                                                 GQAIGSAENLTKGFSNAKTVLSGIQSILGSVLAGMDLDEALQK-NSNELTLAKAGLELTN
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y and Molecular Evolution of
Ovine Strains of Mannheimia
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19,
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Last sequence update)
Last annotation updat
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Pred. No. 5
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                                                                                                                                                                                                                                                                                         Mismatches
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5.4e-97;
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                                                                                                                                                                                                                                                                                                                                            CRC64;
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Query Match
Best Local Similarity
                                        EMBL; AF314518; AAG40302.1; -.
EMBL; AF314517; AAG40301.1; -.
Interpro; IPR001753; Enoyl_Ca_hydrtse.
Interpro; IPR001343; Hemlysn_Ca_bind.
Interpro; IPR003355; RTX_N.
Pfam; PF00353; hemolysinCabind; 1.
Pfam; PF00353; hemolysinCabind; 1.
Pfam; PF00353; CABUNGRPT.
PRONSITE; PR00313; CABUNGRPT.
PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
SEQUENCE 953 AA; 102135 MW; 70DB354157F5881E CR
                                                                                                                                                                                                                                                                                                   Q9ETX2;
01-MAR-2001
01-MAR-2001
01-JUN-2001
                                                                                                                                                         "Sequence diversity and molecular evolution of gene in bovine and ovine strains of Mannheimia haemolytica.";
                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=PH498, AND PH344;
Davies R.L., Whittam T.S
                                                                                                                                                                                                                                                                                                                                                Q9ETX2

    J. Bacteriol. 0:0-0(2001).

                                                                                                                                                                                                                                      NCBI_TaxID=85401;
                                                                                                                                                                                                                                                 Mannheimia.
                                                                                                                                                                                                                                                           Bacteria; Proteobacteria;
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49
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16,
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 Score
Pred.
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                                                                                                                                                                                                                                                            subdivision; Pasteurellaceae;
 No. 6e-97;
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                                            CRC64;
            Length 953
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Matches
    Q9EV25;
Q9EV25;
01-MAR-2001
01-MAR-2001
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                                                                                                                              PRWY----ITSNLQNYQSNKTDHKIEQLIGKDGSYITSDQIDKILQDKKDGTVITSQELK 871
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     (TrEMBLrel.
                                   PRELIMINARY;
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    16,
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PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.

SEQUENCE 953 AA; 102138 MW; C41D9EBC1D799951 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Bacteriol. 183:1394-1404(2001).
EMBL; AF314520; AAG40304.1; -
InterPro; IPR001753; Enoyl_CoA_hydrtse.
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR003355; RTX_N.
Pfam; PF00353; hemolysinCabind; 1.
Pfam; PF02382; RTX; 1.
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Davies R.L., Whittam T.S., Selander R.K.;
"Sequence Diversity and Molecular Evolution of Gene in Bovine and Ovine Strains of Mannheimia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-PH496;
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NCBI_TaxID=85401;
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Bacteria; Proteobacteria;
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                                                                                                                            LEWEKQNGGQNYFDKGYDSRYAAYLANNLKFLSELNKELEAERVIAITQQRWDNNIGELA 462
GTDEIGLIVNAKAGNDDIFYGQGKMNIDGGDGHDRVFYSKDGGFGNITYDGTSATEAGSY
                                                                                  VEWEKNNHGKNYFENGYDARYLANLQDNMKFLLNLNKELQAERVIAITQQQWDNNIGDLA
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Pred. No. 6e-97;
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Q9EV26;
01-MAR-2001
01-MAR-2001
01-DEC-2001
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Bacteria; Proteobacteria;
Mannheimia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Bacteriol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21101823; PubMed=11157953;
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                                                     AKGLDSVENIDRKLGKASNVLSTLSSFLGTALAGIELDSLIKKGDAAPDALAKASIDLIN
                                                                                              LVKAAEELGIEVQKEEGNDIAKAQTSLGTIQNVLGLTERGIVLSAPQLDKLLQK---TKV
                                                                                                               GGKGDDIFVHRQGDGNDIITDSDGNDKLSFSDSNLKDLTFEKVKHNLVI-TNSKKEKVTI
ETIGNLSQSTQTTEAFSSQLAKLGSTTSQAKGFSNTGNKLQNLN-FSKTNLGLETTGLL
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RTX; 1.
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Q9EV32;
Q1-MAR-2001
01-MAR-2001
01-DEC-2001
           MEDLINE=21101823; PubMed=11157953;
Davies R.L., Whittam T.S., Selander R.K.;
"Sequence Diversity and Molecular Evolution
Gene in Bovine and Ovine Strains of Mannheim
                                                                                                                                              Pasteurella haemolytica.
Bacteria; Proteobacteria;
Mannheimia.
                                                                                STRAIN-PH706
                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                               LEUKOTOXIN
                                                                                                                                NCBI_TaxID=75985;
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19,
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Last sequence update)
Last annotation update)
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volution of Mannheimia

the Leukotoxin (Pasteurella)

Pasteurellaceae;

953 ₹

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PRWY----ITSNLQNYQSNKTDHKIEQLIGKDGSYITSDQIDKILQ-----DKKD-GTV
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VDNYELLK-----HSKNVTNSLDKLISSASAFTSSNDSRNVLVAPTSMLDQSL
                                          ITSQELKKLADENKSQKLSASDIASSLNKLVGSMALFGTANSVSSNALQPITQPTQGI 922
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Best Local Similarity
Matches 473; Conserv
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Pfam; PF02382; RTX; 1.
PRINTS; PR00313; CABNDUGRPT.
PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
SEQUENCE 953 AA; 102078 MW; EF425243C8741EE4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF314509; AAG40293.1
InterPro; IPR001753; Enoyl
InterPro; IPR001343; Hemly
InterPro; IPR003355; RTX_N
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 PRWY----ITSNLQNYQSNKTDHKIEQLIGKDGSYITSDQIDKILQDKKDGTVITSQELK
                                      GGAGNDVYIFRKGDGNDTLYDGTGNDKLAFADANISDIMIERTKEGIIVKRNDHSGSINI
                                                          FNDVFKGSKFNDIFHSGEGDDLLDGGAGDDRLFGGKGNDRLSGDEGDDLLDGGSGDDVLN
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                    TVNRFVESGKALHEVTSTHTALVGNREEKIEYR-HSNNQHHAGYYTKDTLKAVEEIIGTS
                                                                                                                        TVNRKVARGDIYHEVVKRQETKVGKRTETIQYRDYELRKVGYGYQSTDNLKSVEEVIGSQ
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49.5%;
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Pred. No. 3.26
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01-MAR-2001
01-MAR-2001
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InterPro; IPR001753; Enoyl_CoA_hydrtse.

InterPro; IPR001343; Hemlysn_Ca_bind.

InterPro; IPR003355; RTX_N.

Pfam; PF00353; hemolysinCabind; 1.

pfam; PF00382; RTX; 1.

PFANT; PF00313; CABNUNGRPT.

PRINTS; PR00313; CABNUNGRPT.

PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.

SEQUENCE 953 AA; 102132 MW; 4138AB5FAE2843B3
                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-21101823; PubMed-11157953;
Davies R.L., Whittam T.S., Selander R.K.;
"Sequence Diversity and Molecular Evolution of
Gene in Bovine and Ovine Strains of Mannheimia
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-PH66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mannheimia.
NCBI_TaxID=75985;
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                                                                                                                                                                AKGLDSVENIDRKLGKASNVLSTLSSFLGTALAGIELDSLIKKGDAAPDALAKASIDLIN
                                                                          GQAIGSAENLTKGFSNAKTVLSGIQSILGSVLAGMDLDEALQK-NSNELTLAKAGLELTN
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TISTALGAVSAGVSAAAVGSAVGAPIALLVAGVTGLISGILEASKQAMFESVANRLQGKI
                                     SLIENIANSVKTLDAFGDQINQIGSKLQNVKGLSSLGDKLKGLSGFDKTSLGLDVVSGLL
                                                                                                                           Similarity
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pred. No. 4e-96;
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Davies R.L., Campbell S., Whittam T.S.;

"Mosaic structure and molecular evolution of the leuk
(lktCABD) of Mannheimia (pasteurella) haemolytica, Ma
glucosida and pasteurella trehalosi.";
J. Bacteriol. 0:0-0(2001).
Z. Bacteriol. 0:0-0(2001).
Z. BHBL; AF314515; AAG40299.1;
Z. EMBL; AF314515; AAG40299.1;
Z. EMBL; AF41411; AAL13281.1;
Z. InterPro; IPR001753; Enoyl_CoA_hydrtse.
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR003355; RTX_N.
Z. Ffam; PF00353; hemolysinCabind; 1.
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SEQUENCE FROM N.A.
STRAIN-PH292, AND PH296;
STRAIN-PH292, AND PH296;
STRAIN-PH292, PubMed=11157953;
MEDLINE=21101823; PubMed=11157953;
Davies R.L., Whittam T.S., Selander R.K.;
Pavine Diversity and Molecular Evolution
"Sequence Diversity and Molecular Evolution
"Sequence Diversity and Molecular Evolution
"Sequence Diversity and Molecular Evolution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9EV28;
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01-MAR-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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Pasteurella
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PRINTS; PR00313; CABNDNGRPT.
PROSSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
SEQUENCE 953 AA; 102218 MW; 04AB1715B819E571
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Best Local Similarity 50.1%;
Matches 465; Conservative 1
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EMBL; AF314507; AAG40281.1; -.

EMBL; AF314506; AAG40280.1; -.

EMBL; AF314506; AAG40290.1; -.

InterPro; IPR001753; Enoy1_CoA_hydrtse.

InterPro; IPR001343; Hemlysn_Ca_bind.

InterPro; IPR003355; FTX_N.

Pfam; PF00353; hemolysinCabind; 1.

Pfam; PF00353; hemolysinCabind; 1.

Pfam; PF00353; RTX; 1.

Pfam; PF00351; CabNDNGRPT.

PRINTS; PR001313; CABNDNGRPT.

PROSITE; PR001313; CABNDNGRPT.

PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.

SEQUENCE 953 AA; 101997 MW; D593D6A577C3ADE9 CRC
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01-MAR-2001
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STRAIN-PH284, PH388, AND PH8;
Davies R.L., Whittam T.S., Selander R.K.;
"Sequence diversity and molecular evolution of the leukotoxin (lktA)
gene in bowine and ovine strains of Mannheimia (Pasteurella)
haemolytica.";
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Bacteria; Proteobacteria;
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                                               AYLANNLKFLSELNKELEAERVIAITQQRWDNNIGELAGITKLGERIKSGKAYADAFEDG
  KKVEAGSNITLDAKTGIIDISNSNGKKTQALHFTSPLLTAGTESRERLTNGKYSYINKLK
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Pred. No. 6.3e-96;
75; Mismatches 263
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RESULT 11
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                                                    Query Match
Best Local Similarity
Matches 469; Conserv
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                                                                                                                     Pfam; PF00353; hemolysinCabind; Pfam; PF02382; RTX; 1. PRINTS; PR00313; CABNDMGRPT. PROSITE; PS00166; ENOYL_COA_HYDE SEQUENCE 953 AA; 102160 MW;
                                                                                                                                                                                                                                                                                                                                                                                       Pasteurellà haemolytica.
Bacteria; Proteobacteria;
Mannheimia.
                                                                                                                                                                                                                                                                           MEDLINE=21101823; pubMed=11157953;
Davies R.L., Whittam T.S., Selander R.K.;
"Sequence Diversity and Molecular Evolution of
Gene in Bovine and Ovine Strains of Mannheimia
                                                                                                                                                                                                                     J. Bacteriol. 183:1394-1404(2001).
EMBL; AF314510; AAG40294.1; -.
InterPro; IPR001753; Enoyl_CoA_hydrtse
                                                                                                                                                                                                                                                                                                                                     STRAIN-PH588;
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                              LEUKOTOXIN.
                                                                                                                                                                                           InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR003355; RTX_N.
                                                                                                                                                                                                                                                               haemolytica.";
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NAGQSLAKAG-QSLKTGAKKIILYIPKDYQYDTEKGNGLQDLVKAAQELGIEVQKEEGND
                        NYIKSNIQAGLNSTKSGLKNLYLAIPKD--YDPQKGGTLNDFIKAADELGIARLAEEPNH
                                                                                                                        PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
953 AA; 102160 MW; A189BF80754A7907 CRC64;
                                                      Conservative
                                                                 50.1%;
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Last sequence up
                                                    Score 2329.5; DB 2
Pred. No. 8.1e-96;
8; Mismatches 259;
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Q9EV27;
Q1-MAR-2001
01-MAR-2001
01-DEC-2001
LEUKOTOXIN.
Pasteurella haemolytica.
Bacteria; Proteobacteria;
Mannheimia.
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                                                                                                            VAAGFELSNQVIGNVTKAISSYVLAQRVAAGLSTTGAVAALITSSIMLAISPLAFMNAAD
                                                                                                                                          R-DDKIEEIIGQNGERITSKQVDELIE--KGNGKIAQSELTKVVDNYQLLKYS-RDASNS
                                                                                                                                                                         TESEGNDKLSFSDSNLKDLTFEKVNHHLVI-TNTKQEKVTIQNWFREAEFAKTIQNYVAT
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19,
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         subdivision;
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annotation
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on update)
         Pasteurellaceae;
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Matches 474
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InterPro; IPR001753; Enoyl_CoA_hydrtse.
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR003355; RTX_N.
Pfam; PF00353; hemolysinCabind; 1.
Pfam; PF00382; RTX; 1.
PRINTS; PR00313; CABNDNGRPT.
PROSITE; PS00106; ENOYL_COA_HYDRATASE; UNKNOWN_1.
SEQUENCE 953 AA; 102230 MW; 2B686808EB370090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Sequence Diversity and Molecular Evolution of Gene in Bovine and Ovine Strains of Mannheimia haemolytica.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21101823; PubMed=11157953; Davies R.L., Whittam T.S., Selande
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-PH392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
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                                                                                                                                                        GOAIGSTENITKGFSNAKIVLSGIQSILGSVLAGMDLDEAL-QNNSNELTLAKAGLELTN
                                                                                                                                                                                                                                                                                                                                                                                                 TVNRFVESGKALHEVTSTHTALVGNREEKIEYR-HSNNQHHAGYYTKDTLKAVEEIIGTS
                  TVNRKVARGDIYHEVVKRQETKVGKRTETIQYRDYELRKVGYGYQSTDNLKSVEEVIGSQ
                                               GTDEIGLIVNAKAGNDDIFVGQGKMNIDGGDGHDRVFYSKDGGFGNITVDGTSATEAGSY
                                                                             TPGTEKRERVQTGKYEYITKLHINRVDSWKITDGAASSTFDLTNVVQRIGIELDNAGNVT
                                                                                        TAGTESRERLTNGKYSYINKLKFGRVKNWQVTDGEASSKLDFSKVIQRV------AETE
                                                                                                                   GISRLGEKVLSGKAYVDAFEEGQHLKADKLVQLDSAKGIIDVSNTGEAKTQHILFRTPLL
                                                                                                                            SGISAGFALADKNASTGKKVAAGFELSNQVIGNVTKAISSYVLAQRVAAGLSTTGAVAAL
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74; Conservative
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Pred. No. 8.1e-96;
0; Mismatches 257
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Q9EV29;
01-MAR-2001
01-MAR-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Davies R.L., Whittam T.S., Selander R.K.; Sequence Diversity and Molecular Evolution of Gene in Bovine and Ovine Strains of Mannheimia haemolytica.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00353; hemolysinCabind; 1.
Pfam; PF02382; RTX; 1.
PRINTS; PR00313; CABNDNGRPT.
PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
SEQUENCE 953 AA; 102147 MW; 11600FDA7849A1CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Bacteriol. 183:1394-1404(2001).
EMBL; AF314514; AAG40298.1; -
InterPro; IPR001753; Encyl_CoA_hydrtse
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR003355; RTX_N.
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Bacteria: Proteobacteria:
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VGAGFELANQVVGNITKAVSSYILAQRVAAGLSSTGPVAALIASTVSLAISPLAFAGIAD
                                  VAAGFELSNQVIGNVTKAISSYVLAQRVAAGLSTTGAVAALITSSIMLAISPLAFMNAAD
                                                                                                                                                                                                                                                                                           VLSTLSSFLGTALAGIELDSLIKKGDAAPDALAKASIDLINEIIGNLSQSTQTIEAFSSQ
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01-MAR-2001
01-DEC-2001
LEUKOTOXIN.
           EMBL; AF314505; AAG40289.1; ...
InterPro; IPR001753; Enoyl_CoA_hydrtse.
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR003355; RTX_N.
                                                                                                          MEDLINE=21101823; PubMed=11157953; Davies R.L., Whittam T.S., Selander R.K.; Davies R.L. Diversity and Molecular Evolution Gene in Bovine and Ovine Strains of Mannheim
                                                                                                                                                                                                                                         Pasteurella haemolytica.
Bacteria; Proteobacteria;
Mannheimia.
                                                                                                                                                                                                                                                                                                                                                        Q9EV34;
01-MAR-2001
                                                                                                                                                                              STRAIN-PH56;
                                                                                                                                                                                           SEQUENCE FROM
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                                                                                           haemolytica.";
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annotation
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PRINTS; PR00313; CABNDNGRPT.
PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
PROSITE: PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
DE48B28EE0EB09FB CRC64;
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                                    HKIEQLIGKDGSYITSDQIDKILQDKKDGTVITSQELKKLADENKSQKLSASDIASSLNK
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75; Mismatches
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1.2e-95;
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Matches 463
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J. Bacteriol. 0:0-0(2001).

EMBL; AF314511; AAG40297.1; -.

EMBL; AF314511; AAG40295.1; -.

Interpro; IPR001753; Enoyl_CoA_hydrtse.

Interpro; IPR001343; Hemlysn_Ca_bind.

Interpro; IPR003355; RTX_N.

Pfam; PF00353; hemolysinCabind; 1.

Pfam; PF02382; RTX; 1.

PRINTS; PR00313; CABANDGRPT.

PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNI
SEQUENCE 954 AA; 102410 MW; 02A60E524.
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SEQUENCE FROM N.A.
STRAIN-PH202, AND PH494;
Davies R.L., Whittam T.S., Selander R.K.;
"Sequence diversity and molecular evolution of "Sequence diversity and molecular evolution of hovine and ovine strains of Mannheimia"
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Q9EUE1;
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01-MAR-2001
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Bacteria; Proteobacteria;
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177; Mismatches 248;
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у	542		594
ъ	560	KLNINRVDSWKITDGEASSTEDLTNVVQRIGIELDNAGNVTKTKETKIIAKLGEGDDNVE	619
γ	595	VGQGKMNIDGGDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNRKVARGDIYHEVVKRQ 6	654
ĕ	620	678 G20 VGSGTTEIDGGEGYDRVHYSR-GNYGALTIDATKETEQGSYTVNRFVETGKALHEVTSTH	78
¥	655	ETKVGKRTETIQYRDYELRKVGYGYQSTDNLKSVEEVIGSQFNDVFKGSKFNDIFHSGEG 7	714
8	679	679 TALVGSREEKIEYRHSNNRQHA-GYYTKDTLTSIEEIIGTSHNDIFKGSQFNDAFNGGDG 737	37
γ	715	DDLLDGGAGDDRLFGGKGNDRLSGDEGDDLLDGGSGDDVLNGGAGNDVYIFRKGDGNDTL 774	74
ğ	738	738 VDTIDGNGGNDRLFGGKGDDIIDGGDGDDFIDGGKGNDLLHGGRGDDIFVHRQGDGNDSI	797
Ŋ	775	YDGTGNDKLAFADANISDIMIERTKEGIIVKRNDHSGSINIPRWYITSNLQNYQSN 830	330
ф	798	ΑŢ	856
Ωy	831	KTDHKIEQLIGKDGSYITSDQIDKILQDKKDGTVITSQELKKLADENKSQKL 882	382
D <sub>0</sub>	857	AKGKDNKIDKNDLANVVNSYELLK	905
Δ.	883	SASDIASSLNKLYGSMALFGTANSVSSNAL 912	
ф	906	NSRNVTNSLDKLISSVSSFTSSND-SRNVL 934	

Search completed: September 11, 2002, 09:01:25 Job time: 283 sec

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90				US-09-124-491-10	S		App
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28	٠			US-07-908-253-3	S		Appl
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44 806	17.3	1794	9	5183745-6	Pa	Patent No.	5183745
45 805.5	17.3	1705	4	US-08-669-785-4	υ.	Sequence	4, Appli
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APPLICANT:	: Hughes,	===	X P	E-LEUKOTOXIN GENE	FUSIONS AND	D	
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ADDRESSEE:	n .	Morrison &	Ğ.	7			
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                                                               Best Local Similarity Matches 465; Conserval
                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION.

APPLICATION NUMBER: US/07/////

APPLICATION 19911016

FILING DATE: 19911016

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Robins, Roberta L.

NAME: Robins, Roberta J.

NAME: ROBINS, ROBER: 33,208
                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1098 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 29
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-327-7250
TELEPAX: 415-327-2951
TELEX: 706141
8 KSNIQAGLNSTKSGLKNLYLAIPKD--YDPQKGGTLNDEIKAADELGIARLAEEPNHTET
                                                               50.2%; Score 2334; DB 1; ilarity 50.1%; Pred. No. 8.8e-175; Conservative 175; Mismatches 263;
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                                                                 Indels 26;
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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US-08-170-126-2
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                                                        Sequence 2, Application Patent No. 5594107
                                                 GENERAL INFORMATION:
APPLICANT: POTTER, APPLICANT: CAMPOS, I APPLICANT: HUGHES, I TITLE OF INVENTION: TITLE OF INVENTION:
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                                                                                                                                 LYGSMALFGTANSVSSNALQPITQPTQGI
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CYTOKINE-CYTOTOXIN
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REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-899
TELEPAX: (415) 627-3231
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
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APPLICATION NUMBER: US 0
ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: US 07/777,715
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STREET: 635 BRY2
CITY: PALO ALTO
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ANLQDNMKFLLNLNKELQAERVIAITQQQWDNNIGDLAGISRLGEKVLSGKAYVDAFEEG
                                                                                      GAPIALLVAGVTGLISGILEASKQAMPESVANRLQGKILEMEKQNGGQNYFDKGYDSRYA 424
                                                                                                                                            HAKSLESYAERFKKLGYDGDNLLAEYQRGTGTIDASVTAINTALAAIAGGVSAAAAGSVI
                                                                                                                                                             HANALDEFAKOFRKFGYDGDHLLAEYQRGVGTIEASLTTISTALGAVSAGVSAAAVGSAV 364
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TELEFAX: (415) 327-3231 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/170
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
ATTORNEY/AGENT INFORMATION:
ANASC. ECEDETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                 REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 900
TELECOMMUNICATION INFORMATION.
TELEPHONE: (415) 617-8999
                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: PALO ALTO
STATE: CALIFORNIA
                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U
ZIP: 94301
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, HUW P.A.
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; LENGTH: 1098 amino ac;
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-954-418-2
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LVGSMALFGTANSVSSNALQPITQPTQGI
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                                                              HKIEQLIGKDGSYITSDQIDKILQDKKDGTVITSQELKKLADENKSQKLSASDIASSLNK 893
                                                                                   TGNDKLAFADANISDIMIERTKEGIIVKRNDHSGSINIPRWY----ITSNLQNYQSNKTD
                                                                                                                                                                                                  VGKRTETIQYRDYELRKVGYGYQSTDNLKSVEEVIGSQFNDVFKGSKFNDIFHSGEGDDL 717
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                                                                                                                                                                                                                                                                                                                                         KHIKADKLVQLDSANGIIDVSNSGKAKTQHILFRTPLLTPGTEHRERVQTGKYEYITKLN
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                                     EKIEETIGQNGERITSKQVDDLI--AKGNGKITQDELSKVVDNYELLKHS-KNVTNSLDK 1060
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465; Conserv
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amino acid
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Pred. No. 8.8e-175;
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APPLICATION NUMBER: US 08/038,
EILING DATE: 29-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33.208
REFERENCE/DOCKET NUMBER: 9000-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 924 amino acids
TYPE: amino acid
TOPOLOGY: 110ear
                                                                                                                                                                                                                                                                                                                               Best Local Similarity Matches 461; Conserv
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APPLICANT: THEISEN, MICHAEL
APPLICANT: HARLAND, RICHARD J.
APPLICANT: RIOUX, CLEMENT R.
TITLE OF INVENTION: VACCINES FOR HAEMOPHILUS SOMNUS
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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STREET: 6
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 VVGNITKAVSSYILAQRVAAGLSSTGPVAALIASTVSLAISPLAFAGIADKFNHAKSLES
                    VIGNYTKAISSYVLAQRVAAGLSTTGAVAALITSSIMLAISPLAFMNAADKFNHANALDE
                                                                IKGLGTLGDKLKNIGGLDKAGLGLDVISGLLSGATAALVLADKNASTAKKVGAGFELANO
                                                                                   AKGFSNIGNKLQNL-NFSKTNLGLEIITGLLSGISAGFALADKNASTGKKVAAGFELSNQ
                                                                                                                                    SVLAGMDLDEAL-QNNSNQHALAKAGLELTNSLIENIANSVKTLDEFGEQISQFGSKLQN
                                                                                                                                                           TALAGIELDSLIKKGDAAPDALAKASIDLINEIIGNLSQSTQTIEAFSSQLAKLGSTISQ
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29-MAR-1993
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2.6e-174;
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                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application Patent No. 5534256
                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
         APPLICATION NUMBER: US/07/908,253
FILING DATE: 1920702
CLASSIFICATION: 420
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                    APPLICANT:
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CITY: PALO ALTO
                                                                                                                                                                                COUNTRY:
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                                                                                                                                                                    9430
                                                                                                                                                                              CALIFORNIA
: UNITED STATES OF AMERICA
ROBINS, ROBERTA L
                                                                                                                                                                                                                             E: ROBERTA L. ROBINS
635 BRYANT STREET
                                                                                                                                                                                                                                                                                                                      HARLAND,
                                                                                                                                                                                                                                                                                                                                        ANDREW A.
                                                                                                                                                                                                                                                                                         RICHARD J.

HAEMOPHILUS SOMNUS OUTER MEMBRANE
PROTEIN EXTRACT ENRICHED WITH IRO
                                                                                                                                                                                                                                                                                                                                                                                  us/07908253
                                                                                            Version
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                                                                                                                                                                                                                                                                                              IRON-REGULATED PROTEINS
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TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 2:
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LENGTH: 926 amino acids
 781
                                                                                                                                  665 IQYRDYELRKVGYGYQSTDNLKSVEEVIGSQFNDVFKGSKFNDIFHSGEGDDLLDGGAGD
                                                                                                                                                                                                                                               543 KITDGAASSTFDLTNVVQRIGIELDNAGNVTKTKETKIIAKLGEGDDNVFVGSGTTEIDG
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                                                                                                                                                                                                                                                                           QVTDGEASSKLDFSKVIQRV-----AETEGTDEIGLIVNAKAGNDDIFVGQGKMNIDG
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VSGITGVISTILQYSKQAMFEHVANKIHNKIVEWEKNNHGKNYFENGYDARYLANLQDNM 422
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FSDSNLKDLTFEKVKHNLVI-TNSKKEKVTIQNWFREADFAKEVPNYKATK-DEKIEEII
                            FADANISDIMIERTKEGIIVKRNDHSGSINIPRWY----ITSNLQNYQSNKTDHKIEQLI
                                                           IEYR-HSNNQHHAGYYTKDTLKAVEETIGTSHNDIFKGSKFNDAFNGGDGVDTIDGNDGN
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50.0%; Pre
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ER: 9000-0026
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Pred. No. 2.66
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US-08-455-970A-2
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                                                                                                                                                                                                                                                     Query Match
Best Local
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07,
EILING DATE: 14-OCT-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-D
SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: REDMOND, MARK J.
APPLICANT: HUGHES, HUW P.A.
TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING
TITLE OF INVENTION: CHIMERAS
                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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 193
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CITY: PALO ALTO
STATE: CALIFORNIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 90
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                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
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                                                                TALAGIELDSLIKKGDAAPDALAKASIDLINEIIGNLSQSTQTIEAFSSQLAKLGSTISQ 192
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AKGFSNIGNKLQNL-NFSKTNLGLEIITGLLSGISAGFALADKNASTGKKVAAGFELSNQ 251
                               SVLAGMDLDEAL-QNNSNQHALAKAGLELTNSLIENIANSVKTLDEFGEQISQFGSKLQN 182
                                                                                                                   VNQFLSLTQTGIAISATKLEKFLQKHSTNKLAKGLDSVENIDRKLGKASNVLSTLSSFLG 132
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                                                                                                  IQTAIGLTERGIVLSAPQIDKLLQK---TKAGQALGSAESIVQNANKAKTVLSGIQSILG
                                                                                                                                                                  LSFPKTGAKKIILYIPQNYQYDTEQGNGLQDLVKAAEELGIEVQREERNNIATAQTSLGT 66
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                                                                                                                                                                                                                                  174; Score 2326.5; C
No. 2.6e-1
174; Mismatches 2
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                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: POTTER
                                                                                                                               APPLICANT: POTTER, ANDREW A.
APPLICANT: REDMOND, MARK J.
APPLICANT: HUGHES, HUW P.A.
TITLE OF INVENTION: GRAH-LEUKOTOXIN CHIMERAS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                               STREET: 635 BRYANT STREET
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF
                                                                                                                       ADDRESSEE:
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                                                                   AMERICA
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Best Local :
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APPLICATION NUMBER: US 07,
FILING DATE: 16-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (415) 327-32: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 926 amino acids
TYPE: amino acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                            TALAGIELDSLIKKGDAAPDALAKASIDLINEIIGNLSQSTQTIEAFSSQLAKLGSTISQ
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                                                                                 GDGHDRVFYSKDGGFGNITVDCTSATEAGSYTVNRKVARGDIYHEVVKRQETKVGKRTET 664
                                                          QVTDGEASSKLDFSKVIQRV----
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                                    KITDGAASSTEDLTNVVQRIGIELDNAGNVTKTKETKIIAKLGEGDDNVFVGSGTTEIDG
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                                                                                                                                                                                   TELEFAX: (415)327-3231
INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
LENGTH: 926 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: POTTER, ANDREW APPLICANT: MANNS, JOHN G. TITLE OF INVENTION: GDRH-
                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)327-3400
                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS LLP
STREET: 285 HAMILTON AVENUE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: MCCRACKEN, THOMAS P.
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CITY: PALO ALTO
                                                                                    Local Similarity
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  73
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 VNQFLSLTQTGIAISATKLEKFLQKHSTNKLAKGLDSVENIDRKLGKASNVLSTLSSFLG 132
                                               LNSTKSGLKNLYLAIPKD--YDPQKGGTLNDFIKAADELGIARLAEEPNHTETAKKSVDT
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                        LSFPKTGAKKIILYIPQNYQYDTEQGNGLQDLVKAAEELGIEVQREERNNIATAQTSLGT
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                                                                        50.1%; Score 2326.5; DB 2; ilarity 50.0%; Pred. No. 2.6e-174; Conservative 174; Mismatches 262;
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09-AUG-1996
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US-08-878-748-6
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                                                                                                           Sequence 6, Application US/08878748 Patent No. 5969126
                                           GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A
APPLICANT: REDMOND, MARK J.
APPLICANT: HUGHES, HUW P.A.
APPLICANT: HUGHES, GRH-LET
           NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & RO
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  635 BRYANT STREET
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FTSSNDSRNVLVAPTSMLDQSL
                                                                                     GQNGERITSKQVDDLI--AKGNGKITQDELSKVVDNYELLKHS-KNVTNSLDKLISSVSA
                                                                                                                                                                            FSDSNLKDLTFEKVKHNLVI-TNSKKEKVTIQNWFREADFAKEVPNYKATK-DEKIEEII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KFLLNLNKELQAERVIAITQQQWDNNIGDLAGISRLGEKVLSGKAYVDAFEEGKHIKADK
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GNRH-LEUKOTOXIN

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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-878-748-6
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: ROBINS, ROBERTA L.
REGISTION NUMBER: 33,208
REFERENCE, DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,156
FILING DATE: 10-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 16-OCT-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 14-OCT-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/779,171

FILING DATE: 16-OCT-1991
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                                                                                                               252
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 423
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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TYPE: amino acid
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                                                                        VIGNVTKAISSYVLAQRVAAGLSTTGAVAALITSSIMLAISPLAFMNAADKFNHANALDE
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                                                                                                                                                                          VVGNITKAVSSYILAQRVAAGLSSTGPVAALIASTVSLAISPLAFAGIADKFNHAKSLES
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IQTAIGLTERGIVLSAPQIDKLLQK---TKAGQALGSAESIVQNANKAKTVLSGIQSILG
                            KFLSELNKELEAERVIAITQQRWDNNIGELAGITKLGERIKSGKAYADAFEDGKKVEAGS
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415) 327-3231
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MOLECULE TYPE:
US-08-535-837-2
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Patent No. 5985289
GENERAL INFORMATION:
                                                                                                  TELEFAX: (415) 327-32
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,83
FILING DATE: 27-SEP-1995
                                                                                                                                  NAME: ROBINS, ROBERTA L.
REGISTON NUMBER: 3,208
REFERENCETON NUMBER: 90
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-3400
                                                                                                                                                                                                               FILING DATE: 27-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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                                                                                  SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
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                                    TOPOLOGY:
                                                                  LENGTH:
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PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                         94301
                                    amino acid
GY: linear
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                                                                  926 amino acids
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HARLAND, RICHARD J.
VENTION: HAEMODHILUS SOMNUS OUTER MEMBRANE
VENTION: PROTEIN EXTRACT ENRICHED WITH IRON-REGULATED PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                       UNITED STATES
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841 GKDGSYITSDQIDKILQDKKDGTVITSQELKKLADENKSQKLSASDIASSLNKLVGSMAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    312 FAKQFRKFGYDGDHLLAEYQRGVGTTEASLTTISTALGAVSAGVSAAAVGSAVGAPTALL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 IKGLGTLGDKLKNIGGLDKAGLGLDVISGLLSGATAALVLADKNASTAKKVGAGFELANQ
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                                                                                                                                                                                                                                                                                                                                   SVLAGMDLDEAL-QNNSNQHALAKAGLELTNSLIENIANSVKTLDEFGEQISQFGSKLQN 182
                                                       FTSSNDSRNVLVAPTSMLDQSL 917
                                                                                    FGTANSVSSNALQPITQPTQGI 922
                                                                                                                         GQNGERITSKQVDDLI--AKGNGKITQDELSKVVDNYELLKHS-KNVTNSLDKLISSVSA
                                                                                                                                                                                           FSDSNLKDLTFEKVKHNLVI-TNSKKEKVTIQNWFREADFAKEVPNYKATK-DEKIEEII
                                                                                                                                                                                                                            FADANISDIMIERTKEGIIVKRNDHSGSINIPRWY----ITSNLQNYQSNKTDHKIEQLI
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50.0%; Pred. No. 2.60
tive 174; Mismatches
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2.6e-174;
les 262;
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Best Local Similarity
Matches 461; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)327-3400
TELEPHAX: (415)327-3231
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 926 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: POTTER, ANDREW APPLICANT: MANNS, JOHN G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 0 FILING DATE: 16-OCT-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 0 FILING DATE: 14-OCT-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
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                                                                                                                       124
                                                                                                                                         133 TALAGIELDSLIKKGDAAPDALAKASIDLINEIIGNLSQSTQTIEAFSSQLAKLGSTISQ 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: MCCRACKEN, THOMAS P.
REGISTRATION NUMBER: 38,548
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CITY: PALO ALTO
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VIGNUTKAISSYVLAQRVAAGLSTTGAVAALITSSIMLAISPLAFMNAADKFNHANALDE
                                                 VNQFLSLTQTGIAISATKLEKFLQKHSTNKLAKGLDSVENIDRKLGKASNVLSTLSSFLG 132
                                                                                                                                                                                           IQTAIGLTERGIVLSAPQIDKLLQK---TKAGQALGSAESIVQNANKAKTVLSGIQSILG
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                                                                                    AKGFSNIGNKLQNL-NFSKTNLGLEIITGLLSGISAGFALADKNASTGKKVAAGFELSNQ 251
                                                                                                                       SVLAGMDLDEAL-QNNSNQHALAKAGLELTNSLIENIANSVKTLDEFGEQISQFGSKLQN
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285 HAMILTON AVENUE,
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SYSTEM: PC-DOS/MS-DOS
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RESULT 11 US-09-124-491-6

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RESULT 12
5476657-3
; Patent No. 5476657
; APPLICANT: POTTER, ANDREW A.
; TITLE OF INVENTION: PASTEURELLA
; COMPOSITIONS AND USES THEREOF
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Best Local
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APPLICATION NUMBER: 504,850
FILING DATE: 05-APR-1990
APPLICATION NUMBER: 335,018
FILING DATE: 07-APR-1989
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CURRENT APPLICATION DATA:
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FILING DATE: 09-FEB-1993
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                                                                                                             Local Similarity
                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                    NO:3:
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'4; Mismatches 262;
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                                                                                                                                         GENERAL INFORMATION:
                          APPLICANT: POTTER, ANDREW A. APPLICANT: REDMOND, MARK J. APPLICANT: HUGHES, HUW P.A. TITLE OF INVENTION: ENHANCED TITLE OF INVENTION: CHIMERAS
         NUMBER OF
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LENGTH: 936 amino acids
TYPE: amino acid
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REFERENCE/DOCKET NUMBER: 9001-0016.10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-CCT-1992
ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Dolor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/455,970A FILING DATE: 31-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                    73 VNQFLSLTQTGIAISATKLEKFLQKHSTNKLAKGLDSVENIDRKLGKASNVLSTLSSFLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
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SVLAGMDLDEAL-QNNSNQHALAKAGLELTNSLIENIANSVKTLDEFGEQISQFGSKLQN
                                           KFLSELNKELEAERVIAITQQRWDNNIGELAGITKLGERIKSGKAYADAFEDGKKVEAGS
                                                                                                      VSGITGVISTILQYSKQAMFEHVANKIHNKIVEWEKNNHGKNYFENGYDARYLANLQDNM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : (415) 327-3400
(415) 327-3231
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Pred. No. 2.66
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2.6e-174;
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RESULT 14
US-08-455-970A-10
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           TELEFAX: (415) 327-323
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: POTTER
                                                               REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-3400
                                                                                                                                                                                CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                  STREET: 200
CITY: PALO ALTO
CTATE: CALIFORNIA
                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: REDMOND, MARK J.
APPLICANT: HUGHES, HUW P.A.
TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING
                                                                                                                                              FILING DATE: 14-OCT-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
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                                                                                                                 REGISTRATION NUMBER:
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 LENGTH:
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SYSTEM: PC-DOS/MS-DOS
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                                               5) 327-3400
327-3231
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                      FGTANSVSSNALQPITQPTQGI 922
                                             GQNGERITSKQVDDLI--AKGNGKITQDELSKVVDNYELLKHS-KNVTNSLDKLISSVSA
                                                                    GKDGSYITSDQIDKILQDKKDGTYITSQELKKLADENKSQKLSASDIASSLNKLVGSMAL
                                                                                                                    FADANISDIMIERTKEGIIVKRNDHSGSINIPRWY----ITSNLQNYQSNKTDHKIEQLI
                                                                                                                                            DRLFGGKGDDILDGGNGDDFIDGGKGNDLLHGGKGDDIFVHRKGDGNDIITDSDGNDKLS
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FTSSNDSRNVLVAPTSMLDQSL 917
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Matches 461
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION UMWBER: US/08/455,970A
FILING DATE: 31-MAY-1995
CLASSIFICATION: 424
DETERMINENT PATENTIAL TAMA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0'
FILING DATE: 14-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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APPLICANT:
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TELEPHONE: (415) 327-3400
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LENGTH: 951 amino acids
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CITY: PALO ALTO
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REFERENCE/DOCKET NUMBER: 90
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VIGNVTKAISSYVLAQRVAAGLSTTGAVAALITSSIMLAISPLAFMNAADKENHANALDE 311
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                                GKDGSYITSDQIDKILQDKKDGTVITSQELKKLADENKSQKLSASDIASSLNKLVGSMAL 900
                                             FSDSNLKDLTFEKVKHNLVI-TNSKKEKVTIQNWFREADFAKEVPNYKATK-DEKIEEII
                      GQNGERITSKQVDDLI--AKGNGKITQDELSKVVDNYELLKHS-KNVTNSLDKLISSVSA 895
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Search completed: September 11, 2002, 08:59:25 Job time: 208 sec

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Post-processing: Minimum Match
Maximum Match
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Leukotoxin 352 pro
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Chimeric protein #
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Bovine IL-2 - LKT
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N-PSDB; AAF57290.
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Minimum DB Maximum DB

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Scoring table: Sequence: Title: Perfect score: Run

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Leukotoxin carrier	AAY33929	20	490	19.3	897.5
Gonadotropin relea	AAY58133	21	695	19.4	901
	AAY58361	21	695	19.4	901
LKT-GnRH chimeric	AAW79573	19	695	19.4	901
LKT-GnRH chimeric	AAW79570	19	544	9.	904.5
Pasteurella haemol	AAE04637	22	450	5	159.5
rrhagi	AAR86998	17	758	9	380.5
urel	AAE04636	22	608	۳	464.5
Ď.	AAR76991	16	1023	7.	1731
uropneumon	AAY51406	21	1022	38.0	767.5
m	AAW22152	18	1022	8	767.5
Leukotoxin AppIIIA	AAR54781	15	1244	1.	1928
A. pleuropneumonia	AAY51412	21	1049		1928
ApxIIIB protein.	AAW22159	18	1049	1.	1928
A. pleuropneumonia	AAY51410	21	956	8.	240.5
ApxIIC protein. A	AAW22156	18	956	ъ.	240.5
APPA haemolysin an	AAR12561	12	956	8	240.5
eukot	AAW07637	17	934	9	301.5
	AAR34548	14	951	9.	312.5
Leukotoxin from P.	AAR15159	12	953	9.	2313
	AAW03945	17	926	9.	317.5
m	AAR10889	12	924	9.	317.5
GnRH-leukotoxin ge	AAR34547	14	936	9.	318.5
n-leuk	AAR34546	14	943	٥.	323.5
urella haen	AAE04638	22	953		2325
PtxA protein of Pa	AAR60072	15	953	0	2325
105kD PTX protein	AAR07167	11	953		2325
	AAB21074	21	1069	0.	326.5
ic protein	AAW13867	18	1069	0	326.5
72	AAR52748	15	1069	0	326.5
chimeric	AAW79569	19	977	0	326.5
otein	AAW03942	17	977	50.1	326.5
352 po	AAW79568	19	926	0	326.5
Recombinant leukot	AAR50291	15	926	50.1	326.5

## ALIGNMENTS

927

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Moraxella; antigen; immune response; infection; RTX toxin; vaccine; antibacterial; A subunit. Novel Moraxella bovis antigen useful in compositions for raising immune response in an animal, has protease, lipase or hemolysin activity (CSIR ) COMMONWEALTH SCI & IND RES (UYME ) UNIV MELBOURNE. 31-AUG-2000; 2000WO-AU01048 Strugnell R, 99AU-0002571. Tennent J; ORG

Result No.

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                                                                                                                                                                                                                                                         NIDGGDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNRKVARGDIYHEVVKRQETKVGK
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                          DKLAFADANISDIMIERTKEGIIVKRNDHSGSINIPRWYITSNLQNYQSNKTDHKIEQLI
                                                                                                                                                                         RTETIQVRDYELRKVGYGYQSTDNLKSVEEVIGSQFNDVFKGSKFNDIFHSGEGDDLLDG
                                                                                                                                                                                                                                    \verb|nidggdghdrvfyskdggfgnitvdgtsateagsytvnrkvargdiyhevvkrqetkvgk|
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Pred. No. 2.4e-294;
0; Mismatches 1;
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22-AUG-1990;
16-OCT-1991;
                                                                                         AAW13866 and AAW13867 represent immunogenic chimeric proteins of the invention. This sequence represents a chimeric protein containing the bovine interleukin-2 (II-2) sequence and a leukotoxin sequence. The chimeric proteins of the invention comprise a cytokine, selected from II-2 and gamma interferon (gamma IFN), linked to at least one RTX toxin epitope (preferably the sequence shown in AAW13865). The RTX toxin used to provide the epitope sequence is preferably a leukotoxin, especially the full-length Pasteurella haemolytica leukotoxin. Alternatively, the leukotoxin is a truncated leukotoxin lacking leukotoxic activity, especially LKT352. The chimeric proteins can be used for the production if vaccines against respiratory diseases such as pneumonia, particularly fibrinous pneumonia caused by P.haemolytica, including shipping fever in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric
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(UYSA-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fibrinous pneumonia;
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DB; AAT60032.
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90US-0571301.
91US-0777715.
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Score 2334; DB 18;
Pred. No. 1.1e-143;
5; Mismatches 263;
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IFN; leukotoxin; pr
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Bovine IL-2; interleukin-2; leukotoxin;
                                      Bovine IL-2/Pasteurella haemolytica leukotoxin fusion protein
                                                                                 19-DEC-2000
                                                                                                                         AAB21073
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                                                                                                                                                                                                                                                                                                                                                                                 immunogenic chimeric protein that comprises gamma-interferon (gamma-IFN) or an active fragment thereof, linked to an epitope of a Pasteurella haemolytica leukotoxin (LKT). Pasteurella species, especially Pasteurella haemolytica, are responsible for respiratory diseases in a range of agricultural animals, most particularly cattle, but also sheep, pigs, horses and fowl. Shipping fever is the most economically important respiratory disease associated with Pasteurella species, affecting 15-30% of exposed cattle and resulting in a 2-5% mortality rate in the exposed population. The vaccine composition of the invention is is useful for preventing or ameliorating respiratory diseases such as pneumonia, particularly shipping fever pneumonia, in livestock. The present sequence represents a fusion protein comprising bovine interleukin-2 (II-2) and Pasteurella haemolytica leukotoxin, which may also be useful for a pasteurella haemolytica leukotoxin, which may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-DEC-1993;
22-JUL-1996;
22-AUG-1990;
16-OCT-1991;
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Chimeric -
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                                                                                                                                                                                                                                                                                                                                                                        also be used as an anti-Pasteurella vaccine.
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N-PSDB; AAQ22771.
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                                                                                          One or more biologically pure antigenic determinants of the leukotoxin protein comprising of at least six amino acids is a component of a new vaccine for animals. The vaccine elicits an enhanced immune response after challenge with Pasteurella haemolytica. The vaccines other component is a bacterial free culture supernatant derived from a culture of Pasteurella
                                                                                                                                                    Claim 1; Figure 1; 40pp; English.
                                                                                                                                                                   Vaccine for preventing Pasteurella haemolytica infections contains leukotoxin protein antigenic determinants and P. haemolytica culture supernatant
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monoclonal; polyclonal; antibody;
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                                                                                                                                                                                                                                                                                                                                                                            This sequence represents a fusion between bovine interleukin-2 (IL2) and Pasteurella haemolytica leukotoxin (LTR). The leukotoxin gene, ltkA, was isolated from a gene library of P. haemolytica by chromosome walking. Immunogenic fusion proteins such as this can be used in vaccine compositions. It can also be used to raise mono-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CIBA )
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16-OCT-1991;
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SASKATCHEWAN.
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                                                                                                               The hmb gene encoding the haemin-binding protein was expressed in E. coli as a fusion to the Pasteurella haemolytica leukotoxin gene lktA coded for by plasmid pAA352. The hmb gene fragment was taken from pRAP504 and starts at the codon for the 33 rd amino acid residue of ORF1. The haemin binding protein can be used in vaccines for preventing or treating H. somnus infections, which cause thromboembolic
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See also AAR42370-86
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Query Match Best Local Similarity 50.0

50.1%; Score 2326.5; 50.0%; Pred. No. 2.80 tive 174; Mismatches

.8e-1

DB 14; Length

924; 25;

Indels

Gaps

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04-JUN-1992;
04-JUN-1992;
04-JUN-1993;
29-MAR-1993;
29-MAR-1993;
29-MAR-1993;
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N-PSDB;
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Rioux C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haemophilus somnus; immunogenic; haemolysin; Lpp
thromboembolic meningoencephalitis; septicaemia;
pneumonia; lktA gene; haemin-binding protein; fu
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See also AAR42370-86
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DB; AAQ51081.
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pr comprise sub-unit antigens from P haemolytica fimbrial protein, pr plasmin receptor, 50 K outer membrane protein and leukotoxin.

XX

Disclosure; Fig 5; 92pp; English.

XX

CC LKT352 is 98% homologous with authentic leukotoxin and migrates contained the LKT352 gene was prepd. as follows: lktA, an Mael fragment conty. the gene was ligated into the Smal site of pUCl3 to form constructs were made in the ptac-based vector, pcH432:lacl digasted with Smal. One, pAA342, consisted of the 5' Ahalil fragment from lktA while the other, pAA345, contained content from lktA while the other, pAA345, contained leukotoxin peptide at high levels while pAA345 expressed full cluctoxin peptide at high levels while pAA345 expressed full cong pield pAA345 was therefore ligated to Styl/BamHI digested pAA342 to yield pAA352 conty. the LKT352 sequence. The protein expressed content peptide antigens, e.g. fimbrial protein, plasmin receptor or 50K outer membrane protein. The vaccines can be used to protect cattle from respiratory diseases such as pneumonia, esp. Sequence 926 AA;

Sequence 926 AA;
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Query Match 50.1%; Score 2326.5; DB 12; Length 926; Best Local Similarity 50.0%; Pred. No. 2.8e-143; Matches 461; Conservative 174; Mismatches 262; Indels 25; Gaps

12;

밁 Š а ρ В Š 밁 δÃ Вр Š В Qy DЬ Ş 밁 δÃ 밁 δÃ В Qy 605 483 492 423 432 372 303 183 124 363 252 193 133 67 73 15 LNSTKSGLKNLYLAIPKD--YDPQKGGTLNDFIKAADELGIARLAEEPNHTETAKKSVDT 7 GDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNRKVARGDIYHEVVKRQETKVGKRTET VIGNVTKAISSYVLAQRVAAGLSTTGAVAALITSSIMLAISPLAFMNAADKFNHANALDE TALAGIELDSLIKKGDAAPDALAKASIDLINEIIGNLSQSTQTIEAFSSQLAKLGSTISQ  $\verb|kitdgaasstfd|| tnvvqrigieldnagnvtktketkilaklgegddnvfvgsgtteildg||$ svlagmdldeal-qnnsnghalakagleltnslieniansvktldefgegisgfgsklqn vvgnitkavssyilaqrvaaglsstgpvaaliastvslaisplafagiadkfnhaksles AKGFSNIGNKLONL-NFSKTNLGLEIITGLLSGISAGFALADKNASTGKKVAAGFELSNO iqtaigltergivlsapqidkllqk---tkagqalgsaesivqnankaktvlsgiqsilg KFLSELNKELEAERVIAITQQRWDNNIGELAGITKLGERIKSGKAYADAFEDGKKVEAGS -AETEGTDEIGLIVNAKAGNDDIFVGQGKMNIDG 664 602 551 482 66 604 542 491 422 431 362 371 311 242 251 72

Дb Qy В Qy 망

В Qy Вр δÃ Dр Qy

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Vector; LKT 352; flanking; recombinant; antigen; somatostatin;
gonadotropin releasing hormone; rotavirus viral protein 4;
carrier protein; lactation; reproduction.
          Gene libraries of P. haemolytica Al (strain B122) were constructed in lambda gtll and pUCl3. Resulting clones were used to transform E. coli and individual colonies were pooled and screened for reaction with serum from a calf which had survived a P. haemolytica infection and that had been boosted with a conc. culture supernatant of P. haemolytica to increase anti-leukotoxin antibody levels. Positive colonies were screened for their ability to produce leukotoxin by incubating cell lysates with bovine neutrophils and measuring the release of lactate dehydrogenase from the neutrophils. A 4kb fragment was obtd. Progressively larger clones were isolated by the produce were isolated by
                                                                                                                                                                                                      Immunological carrier system with enhanced immunogenicity comprises chimeric protein comprising leuco:toxin peptide homologous protein fused to antigen esp. somatostatin or gonadotropin releasing hormone
                                                                                                                                                                                                                                                                                              WPI;
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14-OCT-1992;
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Qy 밁 Qy 밁 20 В Qy В QУ 망 δÃ Qy 뭠 Qy В B 20 В Q DЬ Qy B Qy 밁 Ωy рь δ δ Query Match Best Local Matches 461; in paal14. The clone was subjected to restriction enzyme digestion to yield two clones, one expressing truncated leukotoxin peptide at high levels and the other expressing the full length leukotoxin at low levels. The 3' end of the lkth gene from the full length clone was ligated to the truncated gene clone to yield plasmid pha352. The didner was used to produce chimeric proteins by gene fusion with an antigen coding sequence, e.g. the coding sequence of somatostatin, gonadotrophin releasing hormone or rotavirus viral protein 4, i.e. leukotoxin works as a carrier protein to bring about a larger immune response than the antigen alone. Immunisation with these antigens can regulate growth rate, lactation and reproductive efficiency. See also AAR34546-8. Sequence 303 243 252 124 133 483 492 423 432 363 372 193 543 603 605 552 785 721 725 662 665 67 73 15 LNSTKSGLKNLYLAIPKD--YDPQKGGTLNDFIKAADELGIARLAEEPNHTETAKKSVDT Local Similarity svlagmdldeal-qnnsnqhalakagleltnslieniansvktldefgeqisqfgsklqn 182 TALAGIELDSLIKKGDAAPDALAKASIDLINEIIGNLSQSTQTIEAFSSQLAKLGSTISQ 192 VNQFLSLTQTGTAISATKLEKFLQKHSTNKLAKGLDSVENIDRKLGKASNVLSTLSSFLG 132  ${\tt vvgnitkavs} syila qrva {\tt aglsstgpvaaliastvslaisplafagiadkfnhaksles}$ AKGFSNIGNKLONL-NFSKTNLGLEIITGLLSGISAGFALADKNASTGKKVAAGFELSNO iqtaigltergivls apqidkllqk---tkagqalgsaesivqnankaktvlsgiqsilgQVTDGEASSKLDESKVIQRV------AETEGTDEIGLIVNAKAGNDDIFVGQGKMNIDG kitdgaasstfdltnvvqrlgieldnagnvtktketkiiaklgegddnvfvgsgtteidg gegydrvhysr-gnygaltidatketeggsytvnrfvetgkalhevtsthtalvgnreek GDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNRKVARGDIYHEVVKRQETKVGKRTET  $\tt drlfggkgddildggngddfidggkgndilhggkgddifvhrkgdgndiitdsdgndkls$ DRLFGGKGNDRLSGDEGDDLLDGGSGDDVLNGGAGNDVYIFRKGDGNDTLYDGTGNDKLA IQYRDYELRKYGYGYQSTDNLKSVEEVIGSQFNDVFKGSKFNDIFHSGEGDDLLDGGAGD FADANISDIMIERTKEGIIVKRNDHSGSINIPRWY----ITSNLQNYQSNKTDHKIEQLI ieyr-hsnnqhhagyytkdtikaveeiigtshndifkgskfndafnggdgvdtidgndgn 926 AA; Conservative 50.1%; 174; Mismatches Score 2326.5; DB 14 Pred. No. 2.8e-143; Pred. No. 262; DB 14; Indels Length e digestion peptide at kotoxin at 926; 25; Gaps 123 72 242 431 371 551 482 491 422 362 302 251 661 664 602 604 542 784 720 724

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 Query Match
Best Local Similarity
Matches 461; Conserv
                                                                                                                          Haemophilus somnus enriched with iron regulated proteins is new. The vaccine pref. further comprises an immunogenic leukotoxin polypeptide, esp. an immunogenic Pasteurella haemolytica leukotoxin homologous to LKT352. Example 1.2 describes the prodn. of P. haemolytica recombinant leukotoxin from pAA352.

Two expression constructs were made. One, pAA342, contained the 5'-Ahall fragment of the 1tkA gene, while the other, pAA345, contained the entire 1ktA gene. pAA342 expressed a truncated leukotoxin peptide at high levels, while pAA345 expressed full length leukotoxin at very low levels. Therefore, the 3' end of the 1ktA gene was ligated into pAA342, yielding plasmid pAA352. Or new leukotoxin is 98% homologous to authentic
                                                                                                                                                                                                                                                                                                                                 Haemophilus somnus outer membrane protein extract enriched with iron-regulated proteins, opt. contg
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                                                                                            NB: the protein sequence in Fig 5 comprises 926 amino acids however this protein is described in the text as having
                                                                                                                                                                                                                                                                        A vaccine comprising an outer membrane protein (OMP) extract of
                                                                                                                                                                                                                                                                                                                                                                                                        Harland
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            50.1%;
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  174;
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  Mismatches
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(first entry)
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multimer; vaccine; tumour;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a recombinantly produced or chemically synthesised leukotoxin 352 (LKT 352)polypeptide, derived from the lktA gene that is present in the plasmid pAA352. This gene produces a truncated protein that has an estimated molecular weight of about 99 kDa and lacks the cytotoxic portion of the molecule. Thus this gene has a higher expression level than that of the full-length molecule. This can be used in the construction of a chimeric protein that comprises a leukotoxin polypeptide, several multimers, and a GnRH sequence. The chimeric protein can be used as a vaccine to help reduce the incidence of mammary tumours in a mammalian individual.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A chimeric protein (AAW03942) is composed of a fusion between a truncated leukotoxin (LKT-352) from Pasteurella haemolytica (see also AAW03945) and a 4-copy gonadoliberin-releasing hormone (GnRH) repeat sequence (see also AAW03944). It is the product of a chimeric gene (AAT37176) produced by ligating a synthetic sequence for the 4-copy GnRH into vector pAA52 (ATCC 68283), which carries the LKT-52 gene. Recombinant plasmid pCB113 (LKT 352:4 copy GnRH, ATCC 69749) was obtd. Escherichia coli transformants produced the chimeric protein, which is useful as a vaccine for fertility control, esp. immunological sterilisation of domestic or farm animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gonadotropin-releasing hormone multimer fusion proteins - we leukotoxin polypeptide for increased immunogenicity, useful antifertility vaccine prodn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 7; Fig 5A-5H; 87pp; English.
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kitdgaasstfdltnvvqrigieldnagnvtktketkiiaklgegddnvfvgsgtteidg
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DB; AAT37176.
                            QVTDGEASSKLDFSKVIQRV-----AETEGTDEIGLIVNAKAGNDDIFVGQGKMNIDG
                                                   KFLSELNKELEAERVIAITQQRWDNNIGELAGITKLGERIKSGKAYADAFEDGKKVEAGS
                                                                                                                                                                  VAGVTGLISGILEASKQAMFESVANRLQGKILEWEKQNGGQNYFDKGYDSRYAAYLANNL
                                                                                                                                                                                                   ikglgtlgdklkniggldkaglgldvisgllsgataalvladknastakkvgagfelang
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                                                                                                   kfllnlnkelqaervialtqqqwdnnlgdlagisrlgekvlsgkayvdafeegkhikadk
                                                                                                                                                     vsgitgvistilqyskqamfehvankihnkiveweknnhgknyfengydarylanlqdnm
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Pred. No. 3e-
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The present sequence represents the LKT-GnRH chimeric protein from pCB113. This plasmid contains the LKT-352 polypeptide (AAM79568) fused to four copies of the GnRH peptide. This chimera lacks cytotoxic activity which enables there to be an increase in antigen presentation and thus an optimal immune response. The removal of this region also enables the truncated LKT to be expressed at much higher levels and allows the amount of antigen administered to be reduced. This chimeric protein comprises a leukotoxin polypeptide, several multimers, and a GnR sequence. The chimeric protein can be used as a vaccine to help reduce the incidence of mammary tumours in a mammalian individual.

a GnRH

Chimeric protein of leukotoxin and gonadotropin releasing useful for, e.g. preparation of vaccines for reduction of of mammary tumours in mammals  ${\bf r}$ 

hormone incidence

Figure 5.1-8;

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English.

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kitdgaasstfdltnvvqrigieldnagnvtktketkiiaklgegddnvfvgsgtteidg
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                                                      GKDGSYITSDQIDKILQDKKDGTVITSQELKKLADENKSQKLSASDIASSLNKLVGSMAL 900
                                                                          fsdsnlkdltfekvkhnlvi-tnskkekvtiqnwfreadfakevpnykatk-dekieeii
                                                                                     FADANISDIMIBRTKEGIIVKRNDHSGSINIPRWY----ITSNLQNYQSNKTDHKIEQLI 840
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ftssndsrnvlvaptsmldqsl 917
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Search completed: September 11, 2002, 08:58:47 Job time: 191 sec

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PRINTS; PRO1488; RTXTOXINA.
PROSITE; PS00330; HEMOLYSIN_CALCIUM;
Hemolysis; Toxin; Cytolysis; Cytotox.
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01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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InterPro; IPR003355; RTX_N.
InterPro; IPR003995; RtxA.
                                                                                                                                                                                                                                 MEDLINE-94041617; PubMed-8225575;

BURTOWS L.L., LO R.Y.C., Olah-Winfield E.;

"Molecular analysis of the leukotoxin determinants from Paste haemolytica serotypes 1 to 16.";

Infect. Immun. 61:5001-5007(1993).

-I- PUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK
-I- CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT C
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Bacteria; Proteobacteria;
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                                         ACTIVITY.

DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY) PTM: PALMITOYLATED BY LKTC. THE TOXIN ONLY BECOMES ACTIVE W MODIFIED (BY SIMILARITY).
                                                                                                                                                SUBCELLULAR LOCATION: Secreted.

DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOL
                        SIMILARITY:
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RESULT 3
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TRANSMEM 29 249 POTENTIAL.
TRANSMEM 297 318 POTENTIAL.
TRANSMEM 381 401 POTENTIAL.
DOMAIN 734 784 6 X REPEATS,
REPEAT 734 739 1.
REPEAT 743 748 2.
REPEAT 752 757
REPEAT 750 756 4.
REPEAT 770 775 5.
REPEAT 770 778 6.
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01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation updat
Leukotoxin from serotype All.
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Pfam; PF02382; RTX; 1.
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                                                                                                          SEQUENCE FROM N.A.
STRAIN-SEROTYPE All;
MEDLINE-94041617; PubMed-8225575;
Burrows L.L., Olah-Winfield E., LO R.Y.C.;
Molecular analysis of the leukotoxin determinants
"Molecular analysis of the 10.";
Infect. Immun. 61:5001-5007(1993).
-1- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS TH
                                                                                                                                                                                                                                                                                                                     P55118;
01-OCT-1996
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                                                                                                                                                                                                                                              Pasteurella haemolytica.
Bacteria; Proteobacteria;
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                                                                                                                                                                                                                       NCBI_TaxID=75985;
                                                                                                                                                                                                                                    Mannheimia
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                                          DEFINED.
DEFINED.
SUBCELLULAR LOCATION: Secreted.
SUBCELLULAR LOCATION: Secreted.
DOMAIN: THE GLY-RICH REGION IS
DOMAIN: WHICH IS REQUIRED FOR
DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY) PTM: PALMITOYLATED BY LKTC. THE TOXIN ONLY BECOMES ACTIVE V
                                     ACTIVITY.
                                                                                                CELL MEMBRANES AND CAUSE CELL
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75.0%;
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Pred. No. 9.1;
1; Mismatches
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POTENTIAL.
6 X REPEATS,
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                                                   PROBABLY INVOLVED IN TARGET CELL-BINDING
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LKAA_PASHA
ID LKAA_PA
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DT 30-MAY
DE Leukot
GN LKTA.
OS PASteu
OC Bacter
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Best Local :
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01-OCT-1996 (
01-OCT-1996 (
30-MAY-2000 (
                                                                        MEDLINE-96425875; PubMed-8828217;
Lainson F.A., Murray J., Davies R.C., Donachie W.;
"Characterization of epitopes involved in the neutralization of Pasteurella haemolytica serotype Al leukotoxin.";
Microbiology 142:2499-2507(1996).
-!- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
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SEQUENCE
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                                                                                                                                                                                                                 Bacteria; Proteobacteria; Mannheimia.
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InterPro; IPR003355;
InterPro; IPR003995;
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                                                                                                                                                               STRAIN-SEROTYPE T10;
                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                           Pasteurella haemolytica
                                                                                                                                                                                                                                                                    Leukotoxin
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               SUBCELULAR LOCATION: Secreted. DOMAIN: THE GLY-RICH REGION IS CALCIUM, WHICH IS REQUIRED FOR ACTIVITY.
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   DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED
                                                                 DEFINED.
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6 (Rel. 34, Last sequence update)
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01-APR-1993;
01-APR-1993;
30-MAY-2000;
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01-APR-1993 (Rel. 25, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Hemolysin (Cytolysin II) (CLY-IIA) (HLY-IIA)
APPA OR CLYIIA OR HLYIIA OR CYTC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as your work and for commercial modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                  SEQUENCE FROM N.A. STRAIN=3714;
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                                               -1- SUBCELLULAR LOCATION: Secreted.
-1- DOMAIN: THE GLY-RICH REGION IS
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NCBI_TaxID=716;
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83 403
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75.0%;
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                           REQUIRED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 43; DB Pred. No. 9.1; Mismatches
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POTENTIAL.
6 X REPEATS,
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                           PROBABLY INVOLVED TARGET CELL-BINDIN
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                           CELL-BINDING
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LAR HEMOLYSIN.
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                                                  IN BINDING
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DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY) PTM: PALMITOYLATED BY LYC. THE TOXIN ONLY BECOMES ACTIVE W MODIFIED (BY SIMILARITY). SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY

WHEN

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RESULT 6
RT2A_AGTPL
ID RT2A, A
ID (Cytol)
GN APXIIA
OS ACTINC
OC Bacter
OC ACTINC
OC Bacter
OC ACTINC
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RY (I)
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Best Local Similarity
"heap 9; Conserv
                                                                                                                                                                                                                                                                                                                                               Qy
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             SEQUENCE FROM N.A.
STRAIN-SEROTYPE 5;
MEDLINE-9012633; PubMed=2693022;
Chang Y.-F., Young R., Struck D.K.;
"Cloning and characterization of a he
(Haemophilus) pleuropneumoniae.";
DNA 8:635-647(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane;
TRANSMEM 23
TRANSMEM 30
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PRINTS; PR01488; RTXTOXINA.
PROSITE; PS00330; HEMOLYSIN_0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between
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P15377;
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REPEAT
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REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001343; Hemlysn_Ca_bind
InterPro; IPR003355; RTX_N.
InterPro; IPR003995; RtxA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00353; hemolysinCabind;
Pfam; PF02382; RTX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M90440;
                                                                                                                                                                   01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-II toxin determinant A (APX-IIA) (Hemo.)
(Cytolysin IIA) (CLY-IIA).
APXIIA OR CLYIIA OR HLYIIA OR APPA OR CYTC
                                                                                                                 Bacteria; Proteobacteria; Actinobacillus. ACBI_TaxID=715;
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
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                                                                                                                                                       Actinobacillus pleuropneumoniae
                                                                                                                                                                                                                                                                                                                         455 FLINLNKELQAE 466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                   FLSELNKELEAE 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Toxin;
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                                                                                                                                                                                                                                                              STANDARD;
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Pred. No.
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9 X REPEATS,
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                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                             (Haemophilus subdivision;
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                                        a hemolysin gene from Actinobacillus
                                                                                                                                                                                                                         update)
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                                                                                                                                                                                                             update)
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                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                               pleuropneumoniae)
Pasteurellaceae;
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Best Local
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                                                                                                                                                                                                                                                                                                                                            REPEAT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00353; hemolysinCabind; pfam; PF02382; RTX; 1. PRINTS; PR00313; CABNDNGRPT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There
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-!- SUBCELLULAR LOCATION: Secreted.
-!- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Infect.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cytolysins of Actinobacillus pleuropneumoniae serotype 9.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gielkens A.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Smits M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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PIR; S18853; S18853.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M30602; AAA87232.1; -. EMBL; X61111; CAA43423.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hemolysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001343;
                                    P23448;
01-NOV-1991
                                                                                                BACSU
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  16-OCT-2001
                    01-NOV-1991
                                                                          FLIG_BACSU
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                                                                                                                                                                                                              1 FLSELNKELEAE 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MODIFIED (BY SIMILARITY).
SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sect. Immun. 59:4497-4504(1991).
FUNCTION: ONE OF THE VIRULENCE FACTORS OF WHICH SHOWS A WEAK HEMOLYTIC ACTIVITY AND FOR ALVEOLAR MACROPHAGES AND NEUTROPHILS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CALCIUM, WHICH IS REQUIRED FOR ACTIVITY (BY SIMILARITY).
                                                                                                                                                                          FLINLNKELQAE 466
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                                                                                                                                                                                                                                                  similarity
9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS00330;
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                                                                                                                                                                                                                                                                                                                                                AA;
                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytolysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HEMOLYSIN_CALCIUM;
  20,
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102531 MW;
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                                                                                                                                                                                                                                                                      75.4%;
75.0%;
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                                        Created)
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Cytotoxin;
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8 X REPEATS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9;
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Flagellar motor switch

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RESULT
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Best Local :
                                                                                                                                                         Sus scrofa (Pig).
Eukaryota; Metazoa; (Manumalia; Eutheria; (MCBI_TaxID=9823;
                                                                                                                                                                                                                                                              P0852;
01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Neurofilament triplet M protein (160 kDa neurofilament protein)
(Neurofilament medium polypeptide) (NF-M) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; Q9WY63; 1QC7.
SubtiList; BG10241; flig.
InterPro; IPR000090; Flg_Motor_Flig.
Pfam; PF01706; Flig-C; 1.
PRINTS; PR00954; FLGMOTORFLIG.
Chemotaxis; Flagella; Flagellar rota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptide.";

J. Bacteriol. 173:3573-3579(1991).

T. Bacteriol. ONE OF THE PROTEINS THAT PROPOSED TO BE LOCATED AT THE BASE INTERACTS WITH CHEMOTAXIS PROTEINS CONTACTING COMPONENTS OF THE MOTOR FLAGELLAR ROTATION.
     TISSUB—Spinal cord;
MEDLINS—85076594; PubMed—6439558;
Geisler N., Fischer S., Vandekero
"Hybrid character of a large neur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See ror send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Albertini A.M., Caramori T., Crabb W.D., Scoffone F., Galizzi A.; "The flaA locus of Bacillus subtilis is part of a large operon coding for flagellar structures, motility functions, and an ATPase-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; S14495; S14495.
PIR; B42365; B42365.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Membrane-associated SIMILARITY: BELONGS TO THE FLIG FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSELNPEVQAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSELNKELEAE
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Z99112; CAB13495.1;
  N., Fischer S., Vande character of a large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              338 ĀA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     160
                                                                                                                                                                                 Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        i; Flagellar rotation; Membrane; Complete
38191 MW; 8C44193BA0ADE58E CRC64;
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72.78;
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us group; Bacillus.
                           Vandekerckhove
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Pred. No. 15;
2; Mismatches
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  neurofilament
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15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FORM A SMITCH COMPLEX THAT IS OF THE BASAL BODY. THIS COMPLEX (SUCH AS CHEY) IN ADDITION TO THAT DETERMINE THE DIRECTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ₽
Plessmann U.,
protein (NF-M
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  (NF-M):
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Sus.
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Best Local s
Matches 7
"The bovine neurofilament M subunit has a novel set of KSP repeats normally restricted to NF-H.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, M AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBER.
-i- PTM: THERE ARE A NUMBER OF REPEATS OF THE TRIPEPTIDE K-S-P, NEW PHOSPHORYLATED ON A NUMBER OF THE SERINES IN THIS MOTIF. IT IS
                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001
16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
CARBOHYD
NON_TER
SEQUENCE
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EMBO J. 3:2701-2706(1984).
-i- FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, N
AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBER.
                                                                                                                                            Hill W.D., Zha
Gearhart D.A.;
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Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                Bovidae; Bovinae;
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                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                   Mammalia; Eutheria;
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Intermediate filament; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00038; filament; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FLSELNKELEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTM: PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FUNCTOF THE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H), TH LEVELS OF PHOSPHORYLATION BEING ALTERIAL BEVELOPMENTALLY AND COLNCIDENT WITH A CHANGE IN THE NEUROFILAMENT FUNCTION.

SIMILARITY: BELONGS TO THE INTERNEDIATE FILAMENT FAMILY.

; A05075; OFFCM.
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1 (Rel. 40,
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413
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58.3%;
                                                                                                                                                                 Balin
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Last annotation update)
M protein (160 kDa neurofilament protein)
polypeptide) (NF-M) (Fragment).
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O-LINKED
O-LINKED
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LINKER 1.
COIL 1B.
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                               T.J.,
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                                                                                                                                                               Spicer K.,
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                                                                                                                                                                                                                                  NFM_RAT STANDARD; PRT; 845 AA.
P12839; Q63370;
01-OCT-1989 (Rel. 12, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Neurofilament triplet M protein (160 kDa neurofilament (Neurofilament medium polypeptide) (NF-M).
NEF3 OR NEFM OR NFM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE;
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                                                                                         MEDLINE=87282618; PubMed=2441012;
Napolitano E.W., Chin S.S.M., Colman D.R.,
"Complete amino acid sequence and in vitro
the middle molecular weight neurofilament
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
           STRAIN-WISTAR;
MEDLINE-92332596; PubMed-1321159;
Kelly B.M., Gillespie C.S., Sherm
                                                      SEQUENCE
                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                              NCBI_TaxID=10116;
                                                                                                                                                                                                                   Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THOUGHT THAT PHOSPHORYLATION OF NFH RESULTS IN THE FORMATION OF INTERFILAMENT CROSS BRIDGES THAT ARE IMPORTANT IN THE MAINTENANCE OF AXONAL CALIBER (BY SIMILARITY).

PTM: PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FUNCTIONING OF THE LARGER NEUROFILAMENT POLYPEPTIDES (NE'-M AND NE'-H), THE LEVELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY AND COINCIDENT WITH A CHANGE IN THE NEUROFILAMENT FUNCTION (BY
                                                                                 Neurosci.
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en the Swiss Institute of Bioinformatics and the En
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 C.S., Sherman D.L.,
myelin-forming phen
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LINKER 1.
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8 X 13 AA TANDEM REPEATS.
B8477D85560AC3F6 CRC64;
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                                                                                                            D.R., Liem R.K.H. vitro expression
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                 Brophy P.J.;
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protein NF-M.";
J. Cell Biol. 1
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"Identification of six phosphorylation
tail region of the rat neurofilament pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-92165797;
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EMBL; Z12152; CAA78136.1;
GlycoSuiteDB; P12839; ---
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PTM: PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FUNCTOF THE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H), THE LEVELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY AND COINCIDENT WITH A CHANGE IN THE NEUROFILAMENT FUNCTION.
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FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, M, AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBER. AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEPETIDE K.S.P, NEM IS PHOSPHORYLATED ON A NUMBER OF THE SERINGS IN THIS MOTIF. IT IS PHOSPHORYLATED ON A NUMBER OF NEH RESULTS IN THE FORMATION OF THOUGHT THAT PHOSPHORYLATION OF NEH RESULTS IN THE MAINTENANCE INTERFILAMENT CROSS BRIDGES THAT ARE INDORTANT IN THE MAINTENANCE
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z.-s., Chevrier M.R.,
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01-AUG-1988 (Rel. 08, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Neurofilament triplet M protein (160 kDa neurofilament protein)
(Neurofilament medium polypeptide) (NF-M).
                        DOMAIN
DOMAIN
                                                                                                                                                                Pfam;
                                                                                                                                                                                                                                                            EMBL; X05640; CAA29127.1; -. EMBL; M20481; AAA39815.1; -.
                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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MEDLINE-87158637; PubMed-3103856;
Julien J.-P., Meyer D., Flavell D., Hu
"Cloning and developmental expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-87246694; PubMed-3036526;
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                                                                                                                                             PROSITE;
                                                                                                                 Intermediate filament;
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PTM: THERE ARE A NUMBER OF REPEATS OF THE TRIPEPTIDE K-S-P, NFM IS PHOSPHORYLATED ON A NUMBER OF THE SERIMES IN THIS MOTIF. IT IS THOUGHT THAT PHOSPHORYLATION OF NEH RESULTS IN THE FORMATION OF INTERESTLAMENT CROSS BRIDGES THAT ARE IMPORTANT IN THE MAINTENANCE
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. J. Biochem. 166:71-77(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                           European Bioinformatics Institute.
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FUNCTION: NEUROFILAMENTS
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PTM: PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FUNCTIONING
                                                                                                                                                                                    S00030; S00030.
MGI:97314; Nfm.
rPro; IPR001664; IF.
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Eutheria; Rodentia;
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Sciurognathi; Muridae;
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                                                                                                                    Neurone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hurst J., Grosveld F. on of the murine neuro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DВ
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There are no restrictions
ong as its content is in
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                                                                                                                 Phosphorylation;
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; Murinae; Mus
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P16053;
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sepence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Neurofilament triplet M protein (160 kDa neur
                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restude by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                           +
                                                                                                                                                                                                                                                                                                                                                                                                                                         Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zopf D., Hermans-Borgmeyer I., Gundelfinger E.D., Betz H.; "Identification of gene products expressed in the developing visual system: characterization of a middle-molecular-weight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zopf D., Dineva B., Betz H., Gundelfinger E.D.; "Isolation of the chicken middle-molecular weig (NF-M) gene and characterization of its promote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              neurofilament cDNA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=88112814;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 259-857 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=90174973; PubMed=2106668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Archosauria; Aves;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119
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                                                                                                                                                                                                                                                                                                      IES DEV. 1:699-708(1987).

FUNCTION: NEUROPILAMENTS USUALLY CONTAIN THREE IF PROTEINS: FUNCTION: NEUROPILAMENTS USUALLY CONTAIN THREE IF PROTEINS: AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEUROWAL CALL AND H WHICH ARE A NUMBER OF REPEATS OF THE TRIPEPTIDE K-S-P, PTM: THERE ARE A NUMBER OF THE SERRINES IN THIS MOTIF: IT THOUGHT THAT PHOSPHORYLATION OF NEH RESULTS IN THE FORMATION INTERFILAMENT CROSS BRIDGES THAT ARE IMPORTANT IN THE MAINTE
                                                                                                                                                                   OF AXONAL CALIBER.

PTM: PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FOTHE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H) OF THE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H) LEVELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY COINCIDENT WITH A CHANGE IN THE NEUROFILAMENT FUNCTION. SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OF 259-857 FROM N.A.
88112814; PubMed-3123320;
Hermans-Borgmeyer I., Gu
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; Galliformes; Phasianidae; Phasiani
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EMBL;
PIR; /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NFM_HUMAN
P07197;
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INIT_MET
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                                                                                                                                                                                                                                                                                    MEDLINE=87275853; PubMed=3608989;
Myers M.W., Lazzarini R.A., Lee V.M.-
"The human mid-size neurofilament sub
sequence and the relationship of its
filament gene family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1988 (Rel. 08, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Neurofilament triplet M protein (160 k
(Neurofilament medium polypeptide) (NF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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01-AUG-1988 (Rel. 08,
16-OCT-2001 (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
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                                                                                                                                   "Identification of the major multiphosphorylation neurofilaments.";
                                                                                                                                                                                         SEQUENCE OF ONE OF THE 13 RESIDUE MEDLINE=88158120; PubMed=2450354; Lee V.M.-Y., Otvos L. Jr., Carden
                                                                                                                                                                                                                                                                      EMBO
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
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                                                                                                                   Proc.
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                                                                                                                                                                             azzarini R.A.;
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L; X05558; CAA29073.1;
LAZ7040; AZ7040.
; S08061; S08061.
; S15762; S15762.
     TABLE MEASON SCI. U.S.A. 85:1998-2002(1988).

NAULI ACAD. SCI. U.S.A. 85:1998-2002(1988).

FUNCTION: NEUROPILAMENTS USUALLY CONTAIN THEE IF PROTEINS: L, MEAND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBER, PTM: THERE ARE A NUMBER OF REPEATS OF THE TRIPEPTIDE K-S-P, NFM PHOSPHORYLATED ON A NUMBER OF THE SERINES IN THIS MOTIF. IT IS THOUGHT THAT PHOSPHORYLATION OF THE RESULTS IN THE FORMATION OF INTERFILAMENT CROSS BRIDGES THAT ARE IMPORTANT IN THE MAINTENANCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OR NEFM OR NFM.
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                                                                                                                                                                                                                                                                        6:1617-1626(1987).
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LINKER 2.
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COIL 2B.
O-LINKED (GLCNAC) (HOLDER)
O-LINKED (GLCNAC) (HOLDER)
G -> R (IN REF. 2).
W; 4-E2EOFC6AC64778B (
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Pred. No. 40;
3; Mismatches
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COIL 1A.
LINKER 1.
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Catarrhini; Hominidae
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subunit:
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t: a repeated protein
e to the intermediate
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30-MAY-2000
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SEQUENCE
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                                                                      MEDLINE-93239320; PubMed-8478098;
Chang Y.-F., Ma D.-P., Shi J., Chengappa M.M.;
"Molecular characterization of a leukotoxin ge
haemolytica-like organism, encoding a new memb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
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                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=93239320;
                                                                                                                                                                                                                              Pasteurella haemolytica-like
Bacteria; Proteobacteria; gan
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P55123;
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                                                      family.
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PTM: PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FORM: PHOSPHORYLATION SEEMS TO PLAYEPTIDES (NF-M AND NF-H) OF THE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H) LEVELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY COINCIDENT WITH A CHANGE IN THE NEUROFILAMENT FUNCTION. SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
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A30157; A30157.
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LINKER 12.
COIL 2A.
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COIL 2B.
6 X 13 AA TANDEM RE
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                      CYTOTOXIC
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RTX toxin
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- outstation
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SUBCELLULAR LOCATION: Secreted.

DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING C

OR CYTOLS

CYTOLYTIC

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Best Local
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01-NOV-1997 (Rel. 35, 1
16-OCT-2001 (Rel. 40, I
Hypothetical aldolase c
MJ1418:
SEQUENCE FROM N.A.

STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE-96337999; PubMed-8688087;

MEDLINE-96337999; PubMed-8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
                                                                                                                                                                                                                                                                                                                                                                      REPEAT
REPEAT
SEQUENCE
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                                                                                                       Archaea; Euryarchaeota; Methanococcus.
                                                                                                                                                                                                                       _METJA
                                                                                                                              Methanococcus jannaschii.
                                                                                                                                                                                                 Q58813;
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InterPro; IPR003355;
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ween the Swiss Institute of Bioinformatics
Buropean Bioinformatics Institute. There a
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ACTIVITY.

DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY)
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SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY
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                                                                                                                                                                                                                                                                    458
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35, Last sequence update)
40, Last annotation updat
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3; Cytotoxin;
Palmitate.
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Pred. No. 44;
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7 X REPEAT
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                                                                                                                                                    update)
n MJ1418.
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Job time: 278 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 jannaschii.";
Science 273:1058-1073(1996).
Science 273:1058-1073(1996).
-!- COFACTOR: BINDS ONE ZINC ION PER MOLECULE (POTENTIAL)
-!- SIMILARITY: BELONGS TO THE ALDOLASE CLASS II FAMILY. ARAD/
-!- SIMILARITY: STRONG, TO E.COLI YGBL AND H.INFLUENZAE HIDDL.
SUBFAMILY. STRONG, TO E.COLI YGBL AND H.INFLUENZAE HIDDL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.; "Complete genome sequence of the methanogenic archaeon, Methanococcus tannacchia".
                                                                                                                                                                                                                                                     Hypothetical protein;
METAL 68 87 87
METAL 89 89
                                                                                                                                                                                                                                                                                                                                                               EMBL; U67582; AAB99428.1; -. HSSP; P11550; 3FUA.
                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                          METAL
                                                                                                                                                                                                                                                                                                                    Pfam; PF00596; Aldolase_II;
                                                                                                                                                                                                                                                                                                                                                TIGR; MJ1418;
                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
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                                                                                                           1 FLSELNKELE
                                                                             FLSTINKEIE
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147
              September 11,
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ZINC (BY SIMILARITY).

ZINC (BY SIMILARITY).
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re greater than or equal to the score of the result being poor
is derived by analysis of the total score distribution.
       36
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               protein search, using sw model
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Match
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57
1 FLSELNKELEAE 1
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Minimum Match 0%
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Copyright (c) 1993 - 2000 Compugen Ltd
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QFPGM
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flagellar motor sw
              ribosome
                    unknown protein,
                           hypothetical
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leukotoxin A - Pas
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             receptor,
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- Ent
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ein, 7
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## ALIGNMENTS

leukotoxin A - Pasteurella haemolytica (serotype 1)

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A;Description: lyses leukocytes (C;Superfamily: hemolysin A; hemolysin A homology C;Superfamily: hemolysin A; hemolysis; exotoxin; hemolysis; lipoprotein; tandem rep C;Keywords: calcium binding; cytolysis; exotoxin; hemolysis; lipoprotein; tandem rep F;238-784/Domain: hemolysin A homology <HLYA>
F;716-807/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIYF]-X)
F;554/Binding site: palmitate (Lys) (covalent) #status predicted
В
                                             δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Genetics:
A;Gene: lktA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Rosidues: 1-741,'D',743-953 <LOR>
A;Residues: 1-741,'D',743-953 <LOR>
C;Comment: This organism causes bovine pneumonic pasteurellosis (shipping fever).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 947-953 <STR>
A;Residues: 947-953 <STR>
R;Lo, R;YC.; Strathdee, C.A.; Shewen, P.E.
Infect. Immun. 55, 1987-1996, 1987
A;Title: Nucleotide sequence of the leukotoxin genes
A;Reference number: $29515; MUID:87306837
A;Accession: $29516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-953 <HIG>
R; Strathdee, C.A.; Lo, R.Y.C.
R; Strathdee, C.A.; Lo, R.Y.C.
J; Bacteriol. 171, 916-928, 1989
J; Title: Cloning, nucleotide sequence, and A; Reference number: A32051; MUID:89123172
A; Accession: C32051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: A30169; A; Accession: B30169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N;Alternate names: lktA protein
C;Speckes: Pasteurella haemolytica
C;Date: 12-Oct-1989 #sequence_revision 15-Nov-1996 #text_change 18-Jun-1999
C;Accession: B30169; C32051; S29516
                                                                                                                                                                                                                                                                                                                                                                                                                    C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: not compared with conceptual translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: DNA sequence of the Pasteurella haemolytica leukotoxin gene cluster. A;Reference number: A30169; MUID:89210283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; Highlander, S.K.
DNA 8, 15-28, 1989
                                                                                                       Query Match
Best Local S
Matches S
451 FLINLNKELQAE 462
                                                   \vdash
                                                   FLSELNKELEAE
                                                                                                          Similarity
9; Conserv
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                                                                                                             Conservative
                                                   12
                                                                                                                                   75.4%;
75.0%;
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                                                                                                       Score 43; DB Pred. No. 25; 1; Mismatches
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                                                                                                                                                        Length 953
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C;Function:
A;Description: attacks cell membranes and causes cell lysis
C;Superfamily: hemolysin A; hemolysin A homology
C;Keywords: calcium binding; cytolysis; exotoxin; hemolysis; lipoprotein; tandem repeat;
F;240-786/Domain: hemolysin A homology <HLYA>
F;718-786/Region: repeat
F;718-726/Region: repeat
F;727-735/Region: repeat
F;745-753/Region: repeat
F;745-753/Region: repeat
F;763-771/Region: repeat
F;772-780/Region: repeat
F;781-780/Region: repeat
F;781-809/Region: repeat
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A;Nolecule type: DNA
A;Residues: 950-955 <HIG>
A;Cross-references: GB:M24197; GB:M34943; GB:M34944
A;Cross-references: GB:M24197; GB:M34943; GB:M34944
A;Cross-references: GB:M24197; GB:M34943; GB:M34944
A;Cross-references: GB:M24197; GB:M34944
A;Cross-references: GB:M24197; GB:M34943; GB:M34944
A;Cross-reference EMBL Data Library, June 1993
A;Bescription: DNA sequence of the carboxy terminal end of leukotoxin A from A;Reference number: S34235
A;Recession: S34235
A;Rocession: S34237
A;Rolecule type: DNA
A;Residues: 745-955 CLA22
A;Residues: 745-955 CLA22
toxin II - Actinobacillus pleuropneumoniae
N;Alternate names: cytolysin II; RTX-toxin II (ApxII)
C;Species: Actinobacillus pleuropneumoniae
C;Date: 09-Mar-1990 #sequence_revision 01-Nov-1996 #text_change 18-Jun-1999
C;Accession: B3389; S18853; B43599
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A;Molecule type: DNA
A;Moslecule type: DNA
A;Residues: 723-955 <LA3>
A;Cross-references: EMBL:Z22887; NID:g311824; PIDN:CAA80501.1;
A;Experimental source: serotype T10
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A;Title: Secretion and expression of the Pasteurella haemolytic A;Reference number: A35254; MUID:90236888
A;Accession: A35254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:Z22884; NID:g311828; PIDN:CAA80498.1; PID:g311829 A;Experimental source: serotype T3
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9; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                      464
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75.0%;
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Pred. No.
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25;
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A;Title: Cytolysins of Actinobacillus pleuropneumoniae serotype A;Reference number: A43599; MUID:92040145 A;Accession: B43599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Keywords: Calcium binding; cytolysis; exotoxin; hemolysis; lip F; 243-787/Domain: hemolysin A homology <HLYA>
F; 719-801/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LYIYF]-X)
F; 557/Binding site: palmitate (Lys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X61111; NID:g38939; PIDN:CAA43423.1; PID:g38941 R;Smits, M.A.; Briaire, J.; Jansen, R.; Smith, H.E.; Kamp, E.M.; Gielken Infect. Immun. 59, 4497-4504, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Cloning and characterization of a A;Reference number: A33389; MUID:90126233 A;Accession: B33389
F;243-787/Domain: hemolysin A homology <HLYA>F;719-801/Region: 9-residue repeats (G-G-X-G-F;557/Binding site: palmitate (Lys) (covalent
                                                                                                                                                     A;Experimental source: isolate 3714
A;Note: sequence extracted from NCBI backbone (NCBIN:104212, NCBIP:104211)
C;Comment: This organism causes acute fatal septicemia in young pigs.
C;Function:
                                                                                                                                                                                                                                                                                                      Infect. Immun. 60, 2166-2173, 1992
A;TitLe: Molecular characterization of
A;Reference number: A43834; MUID:922676
A;Accession: A43834
                                                                                                                                                                                                                                                                                                                                                                                                                               N;Alternate names: ashA protein; cytolysin II; RTX-toxin C;Species: Actinobacillus suis C;Date: 31-Dec-1993 #sequence_revision 08-Nov-1996 #text_C;Accession: A43834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db
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A;Gene: apxIIA; appA; clyIIA
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A; Residues: 1-27;948-956 <SM2>
A; Cross-references: GB: X61111; NID: g38939
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A; Residues: 1-956 <SMI>
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A; Accession: $18853
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Smits, M.A.; Briaire, J.; Jansen, R.; Smith, H.E.; submitted to the EMBL Data Library, July 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: serotype 5
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DNA 8, 635-647, 1989
                                                                         C;Superfamily: hemolysin A; hemolysin A homology
C;Keywords: calcium binding; cytolysis; exotoxin; hemolysis; lipoprotein;
                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-956 <BUR>
                                                                                                                              A; Description: attacks cell
                                                                                                                                                                                                                                                                                                                                                                                                          R; Burrows, L.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     toxin II - Actinobacillus suis
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Best Local
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                                                                                                 attacks cell membranes and causes cell lysis hemolysin A; hemolysin A homology
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o
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75.0%;
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Pred. No.
1; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             core 43; DB ced. No. 25; Mismatches
  (G-G-X-G-[DN]-D-X-[LVIYF]-X) (covalent) #status predicted
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F:98-194/Region: coil Ib
F:217-367/Region: coil II
F:400-597/Region: glutamic acid-rich
F:598-674/Region: 6-residue repeats
F:598-674/Region: 6-residue repeats
F:675-784/Domain: carboxyl-terminal #status predicted
F:616,622,628,634,640,646,652,658,670/Binding site: ph
RESULT 7
B42365
flagellar motor
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-784 <LIN>
C:Comment: Neurofilaments are a subgroup of intermediate filaments which are expressed
C:Superfamily: cytoskeletal keratin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neurofilament triplet M protein - Pacific electric ray (fragment)
C:Species: Torpedo californica (Pacific electric ray)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 27-Oct-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Neurochem. 54, 762-770, 1990
A;Title: A unique neurofilament from Torpedo electric
A;Reference number: PN0009; MUID:90155300
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J. Neurochem. 54, 762-770, 1
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A;Molecule type: mRNA
A;Residues: 1-913 <GER>
A;Cross-references: EMBL:U85970; PIDN:AAB53390.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Sequence and expression pattern of two forms A;Reference number: 226090 A;Accession: T52485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neurofilament protein NF-M(2), middle molecular weight [imported] - African clawed C;Species: xenopus laevis (African clawed frog) C;Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 24-Oct-2000 C;Accession: T52485
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nes 8; Conserv
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nes 8; Conservative
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switch protein fliG - Bacillus subtilis
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75.0%;
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Pred. No.
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Pred. No. 35;
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neurofilament triplet M protein - pig (fragments)
N;Alternate names: 160K neurofilament protein; NF-M(medium) protein; type IV IF
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 31-Mar-1988 #sequence_revision 02-Jul-1998 #text_change 10-Jul-1998
C;Accession: A05075; S02570
R;Geisler, N.; Fischer, S.; Vandekerckhove, J.; Plessmann, U.; Weber, K.
EMBO J. 3, 2701-2706, 1984
A;Title: Hybrid character of a large neurofilament protein (NF-M): intermediate
A;Reference number: A05075; MUID:85076594
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: B42365; C69624; S14495
R;Albertini, A.M.; Caramori, T.; Crabb, W.D.; Scoffone, F.; Galizzi, A.
J. Bacteriol. 173, 3573-3579, 1991
A;Title: The flaA locus of Bacillus subtilis is part of a large operon codir
A; Experimental source: spinal cord C; Superfamily: cytoskeletal keratin C; Keywords: blocked amino end; coil
                                                                A; Molecule type: protein
A; Residues: 438-450; 455-459; 460-475; 476-514; 515-532
                                                                                                           A;Title: Location and sequence characterization of the major phosphorylation sites on A;Reference number: S02570; MUID:87304852
A;Accession: S02570
                                                                                                                                                                                 A; Experimental source: spinal cord R; Geisler, N.; Vandekerckhove, J.; Weber, FEBS Lett. 221, 403-407, 1987
                                                                                                                                                                                                                                                      A; Molecule type: protein A; Residues: 1-454 <GEI>
                                                                                                                                                                                                                                                                                                 A; Reference number: A05075; A; Accession: A05075
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C; Keywords: flagellar rotation
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A;Experimental source: strain 168
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A; Residues: 1-338 <ALB>
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A;Accession: B42365
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72.7%;
coiled coil; intermediate filament; phosphoprotein
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Pred. No. 41;
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R;Glasgow, E.; Hall, C.M.; Schechter, N.
J. Neurochem. 63, 52-61, 1994
A;Title: Organization, sequence, and expression of a g
A;Reference number: I50479; MUID:94267484
A;Accession: I50479
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-798 <GLA>
A;Residues: 1-798 <GLA>
A;Cross-references: GB:L09742; NID:g213019; PIDN:AAA72
C;Genetics:
A;Introns: 343/3; 385/2
C;Superfamily: cytoskeletal keratin
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F;99-412/Domain: alpha helical rod <ROD>
F;99-412/Domain: alpha helical rod <ROD>
F;438-454,455-459,460-475,476-514/Domain: tail (fragments) #status predicted <TLP1>
F;515-532/Domain: tail (fragment) #status predicted <TLP2>
F;1/Modified site: blocked amino end (Ser) (probably acetylated) #status experiments
F;456,462,465,479/Binding site: phosphate (Ser) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neurofilament medium protein - goldfish
C;Species: Carassius auratus (goldfish)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 13-Aug-1999
C;Accession: I50479
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                                                                                                                                                            A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-845 < NAP>
Construction of the myelin-forming phenotype express neurofilament protein A; Reference number: $25712; MOID:92332596
A; Accession: $25712; MOID:92332596
A; Accession: $25712; MOID:92332596
               A; Molecule type: mRNA
A; Moslecule type: mRNA
A; Residues: 1-17,19-21, 'P',23-204, 'L',206-500, 'E',501-845 <KEL>
A; Cross-references: EMBL:Z12152; NID:g56751; PIDN:CAA78136.1; PID:g56752
A; Cross-references: EMBL:Z12152; NID:g56751; PIDN:CAA78136.1; PID:g56752
A; Xu, Z.S.; Liu, W.S.; Willard, M.B.
J. Biol. Chem. 267, 4467-4471, 1992
                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Complete amino acid sequence and A;Reference number: A45669; MUID:87282618 A;Accession: A45669
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1e+02;
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A;Reference number: A42393; MUID:92165797
A;Accession: A42393
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Mosiduse: 41-500,'E',501-843,'D' <XUI>A;Note: sequence extracted from NCBI backbone (NCBIP:83873)
C;Superfamily: cytoskeletal keratin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: cytoskeletal keratin C;Keywords: coiled coil; intermediate F;99-244/Domain: coiled coil <CO1> F;267-411/Domain: coiled coil <CO2> F;412-849/Domain: tail <TAI>
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A;Title: Structure and evolutionary origin of the gene encoding A;Reference number: S00030; MUID:87246694
A;Accession: S00030
A;Accession: S00030
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C; Accession: S00030
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N;Alternate names: 160K NF protein; NF-M
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change
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                                                                      A;Cross-references: EMBL:X17102; NID:g63688; PIDN:CAA34958.1; R;Zopf, D.; Dineva, B.; Betz, H.; Gundelfinger, E. submitted to the EMBL Data Library, November 1989
                                                                                                                                                                                                              R;Zopf, D.; Dineva, B.; Betz, H.; Gundelfinger, E.D.
Nucleic Acids Res. 18, 521-529, 1990
A;Title: Isolation of the chicken middle-molecular weight neurofilament (NF-M)
A;Reference number: S15762; MUID:90174973
                                                                                                                                                                                                                                                                                           neurofilament triplet M protein - chicken
C;Species: Gallus gallus (chicken)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
C;Accession: S15762; S08061; A27040
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A; Residues: 1-849 <LEV>
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Eur. J. Biochem. 166,
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A; Molecule type: DNA
A; Residues: 1-355,368-858
                                   A; Reference number: S08061
A; Accession: S08061
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A; Residues: 1-858 <ZOP>
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7; Conserv
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166, 71-77, 1987
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Pred. No. 1.1e
3; Mismatches
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1.1e+02;
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RESULT 14
A64477
L-fuculose-phosphate aldolase homolog - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000
C:Accession: A64477
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, C: Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M. Science 273, 1058-1073, 1996
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.A;Title: Complete genome sequence of the methanogenic archaeon, Methanococc A:Reference number: A64300; MUID:96337999
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C; Superfam1
C; Keywords:
F; 615, 628, 6
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N;Alternate names: NF-M (medlum) protein
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999
C;Accession: A27864; A30157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:Y00067; NID:g35045; PIDN:CAA68276.1; PID:g35046
R;Lee, V.M.Y.; Otvos Jr., L.; Carden, M.J.; Hollosi, M.; Dietzschold, B.; Lazzarini, R.P.
Proc. Natl. Acad. Sci. U.S. A. 85, 1998-2002, 1988
A;Title: Identification of the major multiphosphorylation site in mammalian neurofilamen
A;Reference number: A30157; MUID:88158120
A;Contents: annotation; phosphorylation sites
C;Genetics:
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A;Accession: A27864
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A;Reference number: A27040; MUID:88112814
A;Recession: A27040
A;Molecule type: mRNA
A;Residues: 350-546,'R',548-858 <203>
A;Cross-references: GB:X05558; NID:g63685; PIDN:CAA29073.1; PID:g63686
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C;Superfamily: cytoskeletal keratin
C;Keywords: coiled coil
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A; Residues: 1-916 <MYE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Myers, M.W.; Lazzarini, R.A.; Lee, V.M.Y.; Schlaepfer, W.W.; Nelson, EMBO J. 6, 1617-1626, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:X17102
R;Zopf, D.; Hermans-Borgmeyer, ]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Superfamily: cytoskeletal keratin; Reywords: coiled coil; phosphoprotein; 615,628,641,654,680/Binding site: phosphate
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Similarity 58.3%;
7; Conservative
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58.3%;
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Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 858
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                                                                                 Methanococcus
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                                                                 Smith, H.O.; Woese, which thanococcus jannaschi
                                                                                                                                                          Hurst, M.A.
                                                                                                                                                                                     Sutton, G.G.; Blaick, J.M.; Glodek,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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dek, A.
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Search completed: Job time: 232 sec

September

11,

2002, 09:00:14

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151

LSEEQKELEAE 161

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C.Accession: T03355
R;Crutz-Le Coq, A.M.; Cesselin, B.; Commissaire, J.; Anba, J submitted to the EMBL Data Library, June 1997
A;Description: Sequence and organization of the lactococcal A;Reference number: Z14903
Qγ
                                                                                                         A;Gene: el2
C;Superfamily: Lactococcus phage bIL170 gene el2 protein
                                                                                                                                                                                                                        A; Reference number: A; Accession: T03355
                                                                                                                                                                                                                                                                                                                    gene e12 protein - Lactococcus phage bIL170
C;Species: Lactococcus phage bIL170
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 04-Mar-2000
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T03355
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A;Residues: 1-181 <BUL>
A;Cross-references: GB:U67582; GB:L77117; NID:g1592064; PIDN:AAB99428.1; PID:g159206
                                                                                                                                             C; Genetics:
                                                                                                                                                            A;Cross-references: EMBL:AF009630; NID:g3282260; PIDN:AAC27226.1; PID:g3282307
                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-211 <CRU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Genetics:
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                                                                                                                                                                                                             A;Status:
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2 LSELNKELEAE 12
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7; Conserv
                               similarity
9; Conserv
                                 Conservative
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81.8%;
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                               Score 38; DB Pred. No. 37; O; Mismatches
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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seq length:
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1 FLSELNKELEAE 1
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    BLOSUM62
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 US-08-619-812-8
US-07-908-253-2
US-08-455-970A-2
US-08-387-156-6
US-08-694-865-6
US-08-697-337-2
US-09-124-491-6
5476657-3-370A-12
US-08-455-970A-14
US-08-455-970A-14
US-08-455-970A-14
US-08-455-970A-14
US-08-387-156-8
US-08-177-270A-8
US-08-18-8-1694-65-8
US-08-170-1715-9
US-08-170-1715-9
US-08-170-126-4
US-08-170-126-2
US-08-254-418-2
US-08-215-805A-80
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US-08-215-805A-80
US-08-215-805A-80
US-09-623-618B-21
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Sequence 12, Appli
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Sequence 14, Appli
Sequence 8, Appli
Sequence 14, Appli
Sequence 17, Appli
Sequence 18, Appli
Sequence 2, Appli
Sequence 21, Appli
                                                                                                                                                                                                                                                                                                                                                                                               Description
                                                                                                                        CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/038,719

FILING DATE: 29-MAR-1993

ATTORNEY/AGENT INFORMATION:

NAME: ROBINS, ROBERTA L.

REGISTRATION NUMBER: 33,208

REFERENCE/DOCKET NUMBER: 9000-0019.20

TELEPHONE: (415) 617-8999

TELEPHONE: (415) 327-3231

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 924 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 1
US-08-619-812-8
US-08-619-812-8
; Sequence 8, Application US/08619812
; Patent No. 6100066
; Patent No. 6100066
                                                                                       ; MOLECULE TYPE: US-08-619-812-8
                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/619,812
FILING DATE: 15-MAR-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: POTTER, ANDREW A.
APPLICANT: THEISEN, MICHAEL
APPLICANT: HARLAND, RICHARD J.
APPLICANT: RIOUX, CLEMENT R.
TITLE OF INVENTION: VACCINES FO
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS
STREET: 635 BRYANT STREET
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                 TYPE: amino acid TOPOLOGY: linear
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9; Conserv
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US-08-938-105-3
US-08-310-187A-1
US-08-468-543-10
US-08-469-592-10
US-08-939-046-10
US-07-928-930A-8
US-08-98-930A-8
US-08-98-96-8
US-08-940-95-75
US-08-940-095-119
US-08-940-095-121
US-08-940-093-116
US-08-940-093-116
                            Score 43;
Pred. No.
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Score

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Maximum Minimum

DB BG

Scoring table: Sequence: Perfect score: OM protein -

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FLSELNKELEAE

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US-07-908-253-2

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; MOLECULE TYPE: protein US-07-908-253-2
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Best Local Similarity /3.0
Best Local Similarity /3.0
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 900
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 926 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION: NAME: ROBINS, ROBERTA L.
                                                                                                           APPLICANT: POTTER, ANDREW A.
APPLICANT: REDMOND, MARK J.
APPLICANT: HUGHES, HUW P.A.
TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN
TITLE OF INVENTION: CHIMERAS
                                                                            NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                       424 FLLNLNKELQAE 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 199207 CLASSIFICATION: 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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              CITY: PALO ALTO
STATE: CALIFORNIA
                                                STREET:
                                                                ADDRESSEE:
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635 BRYANT STREET
                                              E: REED & ROBINS
285 HAMILTON AVENUE,
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UNITED STATES OF AMERICA
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PROTEIN EXTRACT ENRICHED WITH IRON-REGULATED PROTEINS
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75.0%;
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        FILING DATA:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-OCT-1992
PRIOR APPLICATION NUMBER: US 07/779,171
APPLICATION NUMBER: US 07/779,171
TTIME DATE: 16-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/08387156 Patent No. 5723129
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Best Local
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INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-OCT-1992
ATTORNEY_AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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APPLICATION NUMBER: US,
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REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-3400
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                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION UMBER: US/08/387,156 FILING DATE: 10-FEB-1995
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424 FLLNLNKELQAE 435
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OPERATING SYSTEM:
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                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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9; Conserv
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amino acid
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HUGHES, HUW P.A.
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                                                                                                                                                                                                                                                                                                     UNITED STATES OF AMERICA
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ROBERTA L.
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REGISTRATION NUMBER:

33,208

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; MOLECULE TYPE: protein US-08-694-865-6
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RESULT
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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INFORMATION FOR SEQ ID NO:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/694,865
                                                                                                                                                                                                                                                                                                                                   FILING DATE: 09-AUG-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: POTTER, ANDREW A. APPLICANY: MANNS, JOHN G. TITLE OF INVENTION: GRH-LEU NUMBER OF SEQUENCES: 34
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MEDIUM TYPE: Floppy
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ADDRESSEE: REED & RO
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                                       424 FLLNINKELQAE 435
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CITY: PALO ALTO
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                                                               1 FLSELNKELEAE 12
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9; Conservative
                                                                                         Similarity 75.0
9; Conservative
                                                                                                                                                                                              amino acids
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(415)307 TO NO: 6:
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                                                                                                      Score 43;
Pred. No.
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Pred. No.
                                                                                         ced. No. 15;
Mismatches
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; MOLECULE TYPE:
US-08-878-748-6
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APPLICANT: POTTER,
APPLICANT: REDMOND
APPLICANT: HUGHES,
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Best Local (
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INFORMATION FOR SEQ ID NO:
                                                                                          APPLICANT: POTTER, APPLICANT: HARLAND, TITLE OF INVENTION: TITLE OF INVENTION:
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APPLICATION NUMBER: US 01
FILING DATE: 10-FEB-1995
                                           NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBERTA L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                         424 FLLNINKELQAE 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: ROBINS, ROBERTA L
REGISTRATION NUMBER: 33
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 19-JUN
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OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: CALIFORNIA
                              STREET:
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9; Conserv
      2: 285 HAMILTON AVENUE, SUITE 200 PALO ALTO
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CALIFORNIA
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                                                                                          HARLAND, RICHARD J.
VENTION: HAEMOPHILUS SOMNUS OUTER MEMBRANE
VENTION: PROTEIN EXTRACT ENRICHED WITH IRON-REGULATED PROTEINS
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                                                                                                                                          POTTER, ANDREW A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTTER, ANDREW A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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75.0%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                       Indels
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy

COUNTRY:

UNITED STATES OF AMERICA

94301

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Best Local Similarity 75.0%;
Matches 9; Conservative
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Patent No. 6022960
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,837
FILING DATE: 27-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 327-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS LLP
STREET: 285 HAMILTON AVENUE, SUITE 200
                                  APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-OCT-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/124,491
                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: GRRH-LEUKOTOXIN CHIMERAS NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: POTTER, ANDREW APPLICANT: MANNS, JOHN G.
                                                                                                    FILING DATE: 10-FEB-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               424 FLINLNKELQAE 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9001-0026.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                     IDR APPLICATION NUMBER: US C. APPLICATION NUMBER: US C. DATE: 09-AUG-1996
""MRER: US 08/387,156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 285 HAM.
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
APPLICATION NUMBER: US 07/779,171 FILING DATE: 16-OCT-1991
                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94301
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Pred. No.
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RESULT 9
5476657-3
; Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: POTTER, ANDREW A.
TITLE OF INVENTION: PASTEURE
COMPOSITIONS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 9
                                                                                                                                                                                                                                                                  US-08-455-970A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO:3:
                                                                                                                                                                                                     Sequence 12, Application US/08455970A
Patent No. 5708155
GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (415)327-3231
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 504,850
FILING DATE: 05-APR-1990
APPLICATION NUMBER: 335,018
FILING DATE: 07-APR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/15,537
FILING DATE: 09-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & RO
                                                                                                                                                APPLICANT: REDMOND, MARK J. APPLICANT: HUGHES, HUW P.A. TITLE OF INVENTION: ENHANCED TITLE OF INVENTION: CHIMERAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      424 FLLNLNKELQAE 435
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                           424 FLLNLNKELQAE 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                           COUNTRY:
                                                                                      STREET:
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amino acid
DGY: linear
                              94301
                                                        PALO ALTO
CALIFORNIA
                                                                                       285 HAMILTON AVENUE,
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                                            UNITED STATES OF AMERICA
                                                                                                        REED & ROBINS
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75.0%;
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75.0%;
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    Mismatches

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Pred. No.
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                                                                                                                                                                 IMMUNOGENICITY USING LEUKOTOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                          SUITE 200
                                                                                                                                                                                                                                                                                                                                                                                                                      6;
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RESULT 11
US-08-455-970A-10
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INFORMATION FOR SEQ ID NO:
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 900
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-3231
                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 07/960,932 FILING DATE: 14-OCT-1992 ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,970A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: REDMOND, MARK J.
APPLICANT: HUGHES, HUW P.A.
TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN
TITLE OF INVENTION: CHIMERAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                        FILING DATE: 31 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                               STREET: 285 HAM:
CITY: PALO ALTO
STATE: CALIFORN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 90
                                                                                                                                                                                                        APPLICATION NUMBER: US/08/455,970A FILING DATE: 31-MAY-1995
                                                                                                                                                                                                                                                                                                                                                          ZIP: 94301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           936 amino acids
                                                                                                                                                                                                                                                                                                                                                                             UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTTER, ANDREW A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                      Floppy disk
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327-3231
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75.08;
                                                           9001-0016.10
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US-08-455-970A-14
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Best Local Similarity 75.0
Matches 9; Conservative
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                                                                                                                        Matches
                                                                                                                                                         Query Match
Best Local
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                                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: lin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 943 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 14-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: REDMOND, MARK J.
APPLICANT: HUGHES, HUW P.A.
TITLE OF INVENTION: ENHANCE
TITLE OF INVENTION: CHIMERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 327-3400
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424 FLININKELQAE 435
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MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC - LOS/MS-DOS
COMPATING SYSTEM: PC-DOS/MS-DOS
COMPATING SYSTEM: PC
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CITY: PALO ALTO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
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                                                                                                                     Conservative
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Pred. No.
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RESULT

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TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 956 amino
                                                                                                                                                                                                                       Sequence 8, Application US/08387156 Patent No. 5723129
                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity Matches 9; Conser
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ADDRESSEE: Bereskin & Parr
STREET: 40 King Street West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 40,261
REFERENCE/DOCKET NUMBER: 65
TELECOMMUNICATION INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Gravelle, Micheline
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                                                                                           APPLICANT: POTTER, ANDREW A.
APPLICANT: REDMOND, MARK J.
APPLICANT: HUGHES, HUW P.A.
TITLE OF INVENTION: GNRH-LEUKOTOXIN CHIMERAS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSE: REED & ROBINS
COMPUTER READABLE FORM
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CITY: T
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Mallard, Bonnie
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                              UNITED STATES OF AMERICA
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Pred. No.
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Best Local :
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INFORMATION FOR SEQ ID NO:
TELEPHONE: (415)327-3400
TELEFAX: (415)327-3231
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/779,171
FILING DATE: 16-0CT-1991
ATTORNEY/AGENT INFORMATION:
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LENGTH: 977 amino acids
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                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0.
CURRENT APPLICATION DATA:
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                                                                                                              APPLICATION NUMBER: US/08/
FILING DATE: 09-AUG-1996
CLASSIFICATION: 424
ATTORNBY/AGENT INFORMATION:
NAME: MCCRACKEN, THOMAS P.
                                 REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 900
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)327-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: POTTER, ANDREW A. APPLICANT: MANNS, JOHN G.
                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: GNRH-LEUKOTOXIN CHIMERAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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COMPOUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-POS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 07/960,932 FILING DATE: 14-OCT-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: ROBINS, ROBERTA L. REGISTRATION NUMBER: 33,
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                                                                                                                                                                                                                                                                                                                                                                               CITY:
                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: REED & ROBINS LLP STREET: 285 HAMILTON AVENUE, SUITE 200
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10-FEB-1995
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                                                                                9001-0016.22
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SEQUENCE CHARACTERISTICS:

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TYPE: maino acids

TYPE: molocov: linear

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lus-08-694-865-8

Query Match
DestLocal Similarity 75.4%: Score 43; DB 2; Length 977;

BestLocal Similarity 75.4%: Score 43; DB 2; Length 977;

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Sequence:
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Copyright (c) 1993 - 2000 Comp
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Q9rcg8 pasteurella
Q93np0 actinobacil
Q46716 escherichia
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Q91c58 escherichia
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Bacteria; Proteobacteria;
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Q99qv5 staphylococ		374	l rat sia	2uv3 rhizobium	Q92kc8 rhizobium m	P96437 rhizobium m	Q9zfg9 azotobacter		Q9r9h2 pseudomonas		Q93npl actinobacil			Q9ev30 pasteurella	029369 archaeoglob		N	4	Q9ev28 pasteurella	Q9ev23 mannheimia	Q9ev25 mannheimia	Q9ev26 mannheimia	Q9ev27 pasteurella	φ	1 pasteurel	N	Q9ev33 pasteurella	Q9ev34 pasteurella

# ALIGNMENTS

19, 19,

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Last sequence update)
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gamma subdivision; Moraxellaceae; Moraxella.

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RESULT
Q43892
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01-NOV-1996
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MEDLINE-21388402; PubMed-11497442;

Angelos J.A., Hess J.F., George L.W.;

Cloning and characterization of a Moraxella bovis cytotoxin gene.";

Am. J. Vet. Res. 62:1222-1228(2001).

EMBL; AF205359; AAK84651.1; -.

EMBL; AF205359; AAK84651.1; -.

SEQUENCE 927 AA; 98845 MW; F4B703577E10A96D CRC64;
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01-MAY-2000
01-MAY-2000
01-JUN-2001
                                                                                                                                                                             Pfam; PF00353; hemolysinGabind; 2.
Pfam; PF00353; RTX; 1.
Pfam; PF02382; RTX; 1.
PRINTS; PR00313; CABNDNGRPT.
PRINTS; PR01488; RTXTOXINA.
PROSITE; PS00330; HEMOLYSIN_CALCIUM; 2.
SEQUENCE 1049 AA; 112308 MW; 9FA5070E48CC3127
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Bacteria; Proteobacteria;
Actinobacillus.
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PRINTS; PRO1488; RTXTOXINA.
PROSITE; PSO0330; HEMOLYSIN_CALCIUM; 3.
SEQUENCE 1055 AA; 113853 MW; 5331C396FA76669E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     in Pasteurella aerogenes.",
Submitted (AUG-1996) to the EMBL/Genl
EMBL; U66588; AAF15370.1; -.
InterPro; IPR001343; Hemlysn_Ca_bind
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STRAIN-FIELD STRAIN JF1319;
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Bacteria; Proteobacteria;
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InterPro; IPR001343; Hem
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LKTA.
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                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heyberger-Meyer B., Frey J., Nicolet Identification and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=749;
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9; Conserv
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L (TrEMBLrel. 17,
                                    Conservative
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a new RTX to
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01-DEC-2001
01-DEC-2001
01-DEC-2001
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Q46716;
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Burland V., Shao Y
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Hall R.H., )
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                                 "The
                                                               Blattner F.R.;
                                                                                                                                                                                           SEQUENCE FROM N.A.
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01-MAY-1999
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                                                                                                                                                                STRAIN-EDL933;
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                                                                                          Shao Y.,
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SEQUENCE FROM N.A.
Shin S.J., Park J.Y., Choi I.S., Sequencing and Sequencing of Apx II.

"Cloning and Sequencing of Apx II.
"Choice of Apx II.
"Ch
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=98290540; PubMed=9628576;
Makino K., Ishii K., Yasunaga T.,
Makino K., Kubota Y., Yamaichi
"Afsudo H.C., Kubota Y., Yamaichi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1999 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
HEMOLYSIN A (HLYA).
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Bacteria; Proteobacteria; gamma
                                                                                                                                                                                                                                                                                                                                                                                 Han C., Ohtsubo A., Kasamatsu M., Hayashi T., Kuhara S., "Complete nucleotide sequences of 93-kb and 3.3-kb plasmienterohemorrhagic Escherichia coli 0157:H7 derived from S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli 0157:H7.
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Escherichia
complete DNA sequence and analysis scherichia coli 0157:H7.";
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                                                                                                                                                                                                    , Xu J., Walderhaug M.O.; (JUL-1994) to the EMBL/G
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                                                                      PubMed=9722640;
Y., Perna N.T.,
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Apx IIIA from Actinobacillus
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Last sequence
Last annotation
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from Sakai
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                                                                                                                                                                                                                                                                                                                                                                                                                    "The enterchemorrhagic Escherichia coli (EHEC) hemolysin Shiga toxin 1 (Stx1) - and Stx2-producing, serotype 0128 E coli strain with a greatest hemolytic activity."; Acta Med. Biol. (Niigata) 0.0-0(2000). EMBL; AB032930; BAA93708.1; -. InterPro; IPR001343; Hemlysn_Ca_bind. InterPro; IPR001343; Hemlysn_Ca_bind. Pfam; PF00353; hemolysinCabind; 2. Pfam; PF02382; RTX_1. Pfam; PF02382; RTX_1.
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HEMOLYSIN.
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Bacteria; Proteobacteria;
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EHEC-HLYA.
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PRINTS; PR01488; RTXTOXINA.
PROSTTE; PS00330; HEMOLYSIN_CALCIUM;
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PROSITE; PS00330; HEMOLYSIN_CALCIUM; 2.
SEQUENCE 998 AA; 107196 MW; CD7A88E9BD862DB6 CRC64;
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EHEC-HLYA.
Escherichia coli.
Bacteria; Proteobacteria;
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SEQUENCE
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MEDLINE-98261495; PubMed-9596716;
Boerlin P., Chen S., Colbourne J.K.,
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EMBL; X79839; CAA56234-1; -.
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR003995; RtxA.
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EMBL; AF043471; AAC24352.1; -.
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"Molecular analysis of the plasmid-encoded hemolysin of Escherichia
coli 0157:H7 strain Ed1933.";
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MEDLINE-97090409; PubMed-8936317;
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Schmidt H.;
Schmidt H.;
Analysis of the EHEC hly operon and its location in fanalysis of the EHEC hly operon and its location in of the large plasmid of enterohemorrhagic Esherichia Microbiology 142:907-914 (1996).
EMBL; X86087; CAA60042.1; -.
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        RESULT 11
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Best Local
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Q51868 PRELIMINARY;
Q51868; Q51866;
01-NOV-1996 (TrEMBLrel. 0
01-NOV-1996 (TrEMBLrel. 0
01-DEC-2001 (TrEMBLrel. 1
LEUKOTOXIN A (FRAGMENT).
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Interpro; IPR003995; RtxA.
Interpro; IPR003355; RTX_N.
pfam; PF00353; hemolysinCabind; 2.
pfam; PF02382; RTX; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Clin. Microbiol. 34:2364-2367(1996).
EMBL; X94129; CAA63849.1; -.
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PRINTS; PR01488; RYXTOXINA.
PROSITE; PS00330; HEMODIXSIN_CALCIUM; 2.
PROSITE: 998 AA; 107255 MW; DA3EF078C7E4131E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21396508; PubMed=11481431;
Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P.,
Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowie A.,
Golding B., Puehler A.;
Golding B., Puehler A.;
"The complete sequence of the 1,683-kb pSymB megaplasmid
fixing endosymbiont Sinorhizobium meliloti.";
Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
EMBL; AL603646; CAC49629.1; -
BMBL; AL603646; CAC49629.1; -
Plasmid; Hypothetical protein; Complete proteome.
glasmid; Hypothetical protein; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhizobium meliloti (Sinorhizobium meliloti).
Plasmid pSymB (megaplasmid 2).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Rhizobiaceae; Sinorhizobium.
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O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL CALCIUM BINDING PROTEIN SMB21402.
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8; Conserv
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57.1%;
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Pred. No.
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Pred. No. 1.6;
2; Mismatches
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Last sequence update)
Last annotation updat
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Best Local S
Matches 7
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Best Local
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STRAIN-T10 SEROTYPE AND T3 SEROTYPE;
Lainson A.F., Altchison K.D., Donachie W.;
Lainson A.F., Altchison K.D., Donachie W.;
Submitted (JUN-1993) to the EMBL/GenBank/DDBJ date EMBL; 222887; CAA80501.1; -.
EMBL; 222887; CAA80501.1; -.
EMBL; 222884; CAA80498.1; -.
HSSP; Q03023; IKAP.
InterPro; IPRO01343; Hemlysn_Ca_bind.
Pfam; PF00353; hemolysinCabind; 1.
PRINTS; PR00313; CABNDWGRPT.
PROSITE; PS00330; HEMOLYSIN_CALCIUM; 2.
NON_TER
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SEQUENCE 233 AA; 25345 MW; AD6C8408731C3F99 C
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Q51865; Q51867;
Q1-NOV-1996 (TIEMBLIEL 01, Create
Q1-NOV-1996 (TIEMBLIEL 01, Last s
Q1-DEC-2001 (TIEMBLIEL 19, Last a
LEUKOTOXIN A (FRAGMENY).
Pasteurella haemolytica.
Bacteria; Proteobacteria; gamma su
Mannheimia.
     Q9EV24
Q9EV24;
01-MAR-2001
01-MAR-2001
01-DEC-2001
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Lainson A.F., Altchison K.D., Donachie W.;
Submitted (JUN-1993) to the EMBL/GenBank/DDBJ
EMBL; 222885; CAA80499 1; -.
EMBL; Z22886; CAA80500.1; -.
HSSP; Q030.3; 1AKL.
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NCBI_TaxID=75985;
[1]
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Bacteria; Proteobacteria;
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nes 7; Conserv
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58.3%;
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Last sequence update)
Last annotation updat
Created)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                           Score 49; DB Pred. No. 1.3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AD6C8408731C3F99 CRC64;
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1.3;
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Q9ETX2;
Q1-MAR-2001
01-MAR-2001
01-JUN-2001
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Davies R.L., Whittam T.S., Selander R.K.;

"Sequence diversity and molecular evolution of the l
gene in bovine and ovine strains of Mannheimia (Past
f haemolytica.";

J. Bacteriol. 0:0-0(2001).

EMBL; AF314518; AAG40302.1; -.

EMBL; AF314517; AAG40301.1; -.

EMBL; AF314517; AAG40301.1; -.

InterPro; IPR001753; Enoyl_CoA_hydrtse.

InterPro; IPR001343; Hemlysn_Ca_bind.

InterPro; IPR00335; RTX_N.

Pfam; PF00353; hemolysinCabind; 1.

Pfam; PF00353; hemolysinCabind; 1.

Pfam; PF00382; RTX; 1.

RRINTS; PR00313; CABBUNGRPT.

RROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.

SEQUENCE 953 AA; 102135 MW; 70DB354157F5881E CRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00353; hemolysinGabind; 1.
Pfam; PF02382; RTX; 1.
PRINTS; PR00318; CABNDWGRPT.
PROSITE; PR00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
SEQUENCE 946 AA; 101480 MW; 25C077858BDC76C4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          haemolytica.";
J. Bacteriol. 183:1394-1404(2001).
EMBL; AF314521; AAG40305.1; ...
Interpro; IPR001753; Encyl_CoA_hydrtse.
Interpro; IPR001343; Hemlysn_Ca_bind.
Interpro; IPR003355; RTX_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Davies R.L., Whittam T.S., Selander R.K.; "Sequence Diversity and Molecular Evolution of Gene in Bovine and Ovine Strains of Mannheimia
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-PH498, AND PH344;
                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Mannheimia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21101823; PubMed=11157953;
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    Similarity 7; Conserv
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7; Conserv
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      Conservative
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Pred. No. 6.4;
3; Mismatches
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core 49; DB red. No. 6.5;
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Search completed: September 11, 2002, 09:01:27 Job time: 285 sec

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Minimum DB
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen
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  AK10_HUMAN
FRPC_HUMAN
CCAB_MOUSE
CCAB_HOUSE
CCAB_HUAN
YM30_YEAST
ABFA_ASPNG
PXA2_YEAST
FOCD_ECOLI
FRPC_HEIMB
YD16_SCHPO
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LKAA_PASHA
RT11_ACTPL
RT12_ACTPL
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RT31_ACTPL
RT32_ACTPL
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AK10_PIG
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23.838 Million cell updates/sec
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P55130 actinobacil
P55131 actinobacil
P08715 escherichia
P16535 pasteurella
P55116 pasteurella
P55117 pasteurella
P55128 actinobacil
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4 rattus norv
5 homo saplen
5 saccharomyc
4 aspergillus
5 saccharomyc
6 escherichia
6 neisseria m
8 archaeoglob
9 schizosacch
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1 actinobacil
7 actinobacil
3 pasteurella
7 proteus mir
6 pasteurella
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Result No.

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37	37	37	37.5	37.5	38	38	38	38	38	38	38
48.1	48.1	48.1	48.7	48.7	49.4	49.4	49.4	49.4	49.4	49.4	49.4
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SYS_PYRAB	NODA_MOUSE	PHLC_STAAU	LON_MYCGE	TKTC_METJA	FRPA_NEIMB	FRPA_NEIMC	CLPE_LACLC	METX_YEAST	JI60_HORVU	ALF_CAMJE	CAPA_CAEEL
Q9uz21 pyrococcus	P43021 mus musculu	P09978 staphylococ		Q58092 methanococc		P55126 neisseria m	Q9s5z2 lactococcus	Q04533 saccharomyc		P53818 campylobact	P34685 caenorhabdi

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPEAT
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                                                                                                                                                                            MEDLINE=93263992; PubMed=8494611;
Chang Y.-F., Shi J., Ma D.-P., Shin S.J.,
"Molecular analysis of the Actinobacillus
                                                                                                                                                                                                                                                                                                                                                    ACTPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR01488; I
PROSITE; PS00330;
                                                                  operons: characterization of the ApxIII operons: Infect. Immun. 62:4411-4418(1994).
-!- FUNCTION: DOES NOT HAVE HEMOLYTIC ACTIVITY
                                                                                                                        SEQUENCE OF 828-1049 FROM N.A. STRAIN=1536 / SEROTYPE 2; MEDLINE=95012630; PubMed=7927703;
                                                                                                                                                                                                                                                                                   RTX-III toxin de IIIA) (CLY-IIIA)
                                                                                                       Jansen R.,
Smits M.A.
                                                                                                                                                            toxin-III gene cluster.";
DNA Cell Biol. 12:351-362(1993).
                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-SEROTYPE 2;
                                                                                                                                                                                                                                                       Actinobacillus pleuropneumoniae
Bacteria; Proteobacteria; gamma
                                                                                                                                                                                                                                                                           APXIIIA OR CLYIIIA OR RTXA OR PTXA
                                                                                                                                                                                                                                    NCBI_TaxID=715;
            ÷
                                                                                               "Genetic map of the Actinobacillus
                                                                                                                                                                                                                                               Actinobacillus.
                                                                                                                                                                                                                                                                                                                                                                                       734
                                                                                                                                                                                                                                                                                                                                                                                                         1 FNDIFHSGEGDDLL
 CYTOTOXICITY TOWARDS ALVEOLAR MACROPHAGES SUBCELLULAR LOCATION: Secreted.

DOMAIN: THE GLY-RICH REGION IS PROBABLY IN CALCIUM, WHICH IS REQUIRED FOR TARGET CELL ACTIVITY (BY SIMILARITY).

DOMAIN: THE THREE TRANSMEMBRANE DOMAINS AR INVOLVED IN PORE FORMATION BY THE CYTOTOXI
                                                                                                                                                                                                                                                                                                                                                                                      FNDVFHGHDGDDLI 747
                                                                                                                R., Briaire J., van
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9; Conser
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                                                                                                                                                                                                                                                                                             determinant A from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RTXTOXINA
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;; Cytotoxin;
Palmitate.
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Pred.
3; Mis
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X
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12.
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                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                       (Haemophilus subdivision;
                                                                                                                 А.В.М.,
                                                                                                                                                                                                                                                                                            serotype 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38DF9AA24649F662 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                     59; DB 1;
No. 0.032;
                              PROBABLY INVOLVED IN TARGET CELL-BINDING
                                                                                       pleuropneumoniae
nxIII operons.";
                                                                                                                                                                                                                                                                                                                                            1049 AA
    CYTOTOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Repeat; Calcium;
                                                                                      operons.
                                                                                                                 Kamp
                                                                                                                                                                                Lein D.H.; pleuropneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLY-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                μ,
                                                                                                                                                                                                                                                                                               (APX-IIIA)
              ARE
                                                                                                                                                                                                                                                          pleuropneumoniae)
pasteurellaceae;
                                                                                                                  Ε.Μ.,
                                                            AND
                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1050;
                                                                     BUT
    (BY
              BELIEVED TO
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                                                            NEUTROPHILS
                                                                                                                  Gielkens A.L.J.,
   IEVED TO BE SIMILARITY).
                                                                                                RTX-toxin
                                                                                                                                                                                                                                                                                               (Cytolysin
                                 OR CYTOLYTIC
                                          BINDING
                                                                     STRONG
                                                                                                                                                                                  RTX
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Best Local
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between
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PROSITE; PS00330; HEMOLYSIN_CALCIUM;
Toxin; Cytolysis; Cytotoxin; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (for send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lipoprotein; TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00313; CABNDNGRPT. PRINTS; PR01488; RTXTOXINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPROUIS45,
InterPro; IPRO03355;
                                                                                                                                                                                                                                                                                                                                    REPEAT
SEQUENCE
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REPEAT
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REPEAT
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Pfam; PF02382; RTX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute.
                                                                             Bacteria; Proteobacteria; gamma subdivision; Actinobacillus.
NCBI_TaxID=715;
                                                                                                                                                   01-OCT-1996 (Rel.
01-OCT-1996 (Rel.
30-MAY-2000 (Rel.
                                                                                                                                                                      P55131;
01-OCT-1996
                                                                                                                                                                                                      ACTPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
                                                                                                                      IIIA) (CLY-IIIA).
APXIIIA OR CLYIIIA OR RTXA OR PTXA.
                                                                                                                                           RTX-III toxin
                                                                                                                                                                                                                                                                                                                                                         REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
operons:
                     Smits M.A.;
                            Jansen R., Briaire
                                        STRAIN=405 / SEROTYPE MEDLINE=95012630; Publ
                                                                                                             Actinobacillus pleuropneumoniae
                                                                                                                                                                                            RT32_ACTPL
        "Genetic map of the Actinobacillus pleuropneumoniae
                                                            SEQUENCE
                                                                                                                                                                                                                                            747
                                                                                                                                                                                                                                                               1 FNDIFHSGEGDDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTM: PALMITOYLATED BY APXIIIC. MODIFIED (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the El
                                                                                                                                                                                                                                             FRDIFHGADGDDLL
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                                                                                                                                                                                                                                                                                   l Similarity
10; Conser
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IPR001343; Hemlysn_Ca_bind.
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3154 371

317 413

397 413

397 413

753 758

762 767

771 775

789 794

789 794

789 794

789 812

807 812

807 831

808 831

808 840

843 849

858 858
                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                         Rel. 34, Last sequence update)
Rel. 39, Last annotation update)
determinant A from serotype 8 (
                                                            N.A.
                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                      AA;
                                                                                                                                                   34,
39,
                                        TYPE 8;
PubMed=7927703;
                              J.,
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                                                                                                                                                                                                                                                                                                                                        112491
                                                                                                                                                                        Created)
                              van Geel A.B.M., Kamp E.M., Gielkens A.L.J.,
  of the
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11 X REPEATS,
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                                                                                                              (Haemophilus
   ApxIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THE TOXIN ONLY BECOMES ACTIVE WHEN
                                                                                                                                                                                             1052 AA

 Calcium;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             There are no rest
  operons.";
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                                                                                                                                            (APX-IIIA) (Cytolysin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Usage
                                                                                                     pleuropneumoniae).
Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane;
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             RTX-toxin (Apx)
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MBL outstation -
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HLYA_ECOLI STANDARD;
P08715;
01-JAN-1988 (Rel. 06, Created)
                                       ECOLI
                                                                                                                                                                                                                                                                                                                                                                                 Lipoprotein;
TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00353; hemolysinCabind; Pfam; PF02382; RTX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001343; Hemlysn_Ca_bind
InterPro; IPR003355; RTX_N.
InterPro; IPR003995; RtxA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00330; HEMOLYSIN_CALCIUM; Toxin; Cytolysis; Cytotoxin; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Cloning and characterization of the Actinobacillus pleuropneumoniae-RTX-toxin III (ApxIII) gene.";
                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Infect.
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                                                                                      748
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SUBCELLULAR LOCATION: Secreted.

DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYT ACTIVITY (BY SIMILARITY).

DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY).

PTM: PALMITOYLATED BY APXIIIC. THE TOXIN ONLY BECOMES ACTIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through a collaboratic ween the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTM: PALMITOYLATED BY APXIIIC. THE TOXIN ONLY BECOMES AC MODIFIED (BY SIMILARITY).
SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ect. Immun. 61:947-954(1993).
FUNCTION: DOES NOT HAVE HEMOLYTIC ACTIVITY
CYTOTOXICITY TOWARDS ALVEDLAR MACROPHAGES I
                                                                                      FRDIFHGADGDDLL
                                                                                                            FNDIFHSGEGDDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X80055; CAA56358.1;
X68815; CAA48711.1;
                                                                                                                                     Similarity
10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    requires a license agreement
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Briaire J., Kamp E.M.,
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275
372
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71.4%;
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                                                                                                                                    Score 58; DB 1;
Pred. No. 0.047;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                               REPEATS, GLY-RICH.
                                                                                                                                                                                                 F83AFE25A6FD8758 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gielkens A.L.J.,
                           1024
                                                                                                                                                                                                                                                                                                                                                                                                           3.
Calcium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (See http://www.isb-sib.ch/announce/
                          AA
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                                                                                                                                                            Length 1052;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRONG
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                                                                                                                                     Gaps
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   the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                         DOMAIN
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stanley P., Packman L.C., Koronakis V., Hughes C. "Fatty acylation of two internal lysine residues toxic activity of Escherichia coli hemolysin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1988 (Rel. 01-MAR-2002 (Rel.
  REPEAT
REPEAT
                                                                                               PROSITE; PS00330; HEMOLYSIN_CALCIUM; 4. Hemolysis; Toxin; Cytolysis; Cytotoxin; Repeat Transmembrane; Lipoprotein; Palmitate; Plasmid
                                                                                                                                                                                                                                                                                                                    This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria;
                                                                                                                                    PRINTS; PR00313; CABNDNGRP PRINTS; PR01488; RTXTOXINA
                                                                                                                                                             Pfam; PF02382; RTX;
                                                                                                                                                                                                                        EMBL; M14107; AAA98233.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PALMITOYLATION OF LYS-564 AND LYS-690
MEDLINE-96404790; PubMed-8808931;
Ludwig A., Garcia F., Bauer S., Jarch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PALMITOYLATION OF LYS-564 AND LYS-690 MEDLINE=95099325; PubMed=7801126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                            TRANSMEM
                                                                          TRANSMEM
                                                                                   TRANSMEM
                                                                                                                                                                                 InterPro; IPR003995;
                                                                                                                                                                                              InterPro; IPR001343; InterPro; IPR003355;
                                                                                                                                                                                                                                                                                                          between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia col
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Analysis of the in vivo activation of hemolysin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEMS Microbiol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

**REOS J., Wels W., Vogel M., Goebel W.;

**Pucleotide sequence of a plasmid-encoded hemolysin determinant and its comparison with a corresponding chromosomal hemolysin sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteriol. 178:5422-5430(1996).
- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD
                                                                                                                                                                                                                                                                                           ween the Swiss Institute of Bioinfo
European Bioinformatics Institute
                                                                                                                                                                                                                                                                                                                                                                      MODIFIED.

DISEASE: THE HEMOLYSIN OF E.COLI IS PRODUCED PREDOMINANTLY STRAINS CAUSING EXTRAINTESTINAL INFECTIONS, SUCH AS THOSE (
                                                                                                                                                                                                                                                                                                                                                                                                                                             CALCIUM,
ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Secreted DOMAIN: THE GLY-RICH REGION IS
                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED INVOLVED IN PORE FORMATION BY THE CYTOTOXIN.

PALMITOYLATED BY HLYC. THE TOXIN ONLY BECOMES AC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                      PF00353; hemolysinCabind;
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Last annotation updat
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                                                                                                            Repeat; Calcium;
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REPEAT
                                                                                                                                             SEQUENCE OF 884-953 FROM N.A.
STRAIN-SEROTYPE AI / PHILIO1;
MEDIINE=90236888; PubMed=2185213;
Highlander S.K., Engler M.J., Weinstock G.M.;
"Secretion and expression of the Pasteurella haen
"Secre
                                                                                                                                                                                                                                                                                                                                                                                                                              "Nucleotide sequence of the leukotoxin haemolytica Al.";
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Highlander S.K., Chidambaram M., Engler M.J., Weinstock
"DNA sequence of the Pasteurella haemolytica leukotoxin
                                                                                                                                                                                                                                                                                                                                                                         [2]
SEQUENCE FROM N.A.
STRAIN-SEROTYPE A1 / PHL101;
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30-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=75985;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria;
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      PTM: PAL
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                                 ACTIVITY.

ACTIVITY.

DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                           Immun.
    PALMITOYLATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proteobacteria;
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(Rel. 15, Last seq
(Rel. 39, Last ann
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MW; 83944917F76C945B CRC64;
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                     THE
                                                                                   PROBABLY INVOLVED TARGET CELL-BINDIN
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[13
                       TOXIN ONLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          of Pasteurella
                                                                                                                                                                                                 haemolytica Leukotoxin.";
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                       ACTIVE
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                                                                                      CYTOLYTIC
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RESULT 6
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REPEAT
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
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DOMAIN
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Pfam; PF00353; hemolysinCabind;
Pfam; PF02382; RTX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; S29516; S29516.
HSSP; P02392; 1CTF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between the Swiss Institute of Bioinfi
the European Bioinformatics Institute.
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                                                                                                                                                                                             P55118;
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                Burrows L.L., Olah-Winfield E., IO R.Y.
"Molecular analysis of the leukotoxin c'
haemolytica serotypes 1 to 16.";
Infect Immun. 61:5001-5007(1993).
-i- FUNCTION: BACTERIAL HEMOLYSINS ARE
CELL MEMBRANES AND CAUSE CELL RUPPU
                                                                                                                                                                           01-OCT-1996
30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003355;
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                                                                        SEQUENCE FROM N.A.
STRAIN-SEROTYPE A11;
MEDLINE=94041617; PubMed=8225575;
                                                                                                                                    Bacteria;
                                                                                                                                                          LKTA.
                                                                                                                            Mannheimia
                                                                                                                                               Pasteurella
                                                                                                                                                                   Leukotoxin
                                                                                                                                                                                                                  LKAB_PASHA
                                                                                                                 NCBI_TaxID=75985;
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SUBCELLULAR LOCATION:
          DEFINED
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Lipoprotein; Palmitate.
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58.3%;
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                                                                                                                                                                    A11.
Secreted
                                                                                                                                     gamma
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                                                                                                                                                                                                                                                                                                                                                      FEHVAN -> LSTLQI (IN D -> Y (IN REF. 2). 7F93D113A118C05F
                                                                                                                                                                                                                                                                                                                Score 49; DB
Pred. No. 1.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                          X REPEATS,
                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                       subdivision;
                   S ARE EXOTOXINS THAT ATTACK BLOOD RUPTURE BY MECHANISMS NOT CLEARL'
                                                                                                                                                                             on update)
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                                                          c.C.;
determinants
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                                                                                                                                        Pasteurellaceae;
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                                                                                                                                                                                                                                                                                                                          Length 953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Calcium;
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RESULT 7
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Matches 7
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P55117;
01-OCT-1996
01-OCT-1996
30-MAY-2000
SEQUENCE FROM N.A.

STRAIN-SEROYVEE T10;

MEDLINE-96425875; Pubmed-8828217;

LAINSON F.A., Murray J., Davies R.C., Donachie W.;

LAINSON F.A., Murray J. Davies R.C., Donachie W.;

"Characterization of epitopes involved in the neutralization of Pasteurella haemolytica serotype Al leukotoxin.";

Microbiology 142:2499-2507(1996).

-1- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00353; hemolysinCabind; Pfam; PF02382; RTX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001343; Hemlysn_Ca_bind. InterPro; IPR003355; RTX_N.
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                                                                                                                                                                                                                       NCBI_TaxID=75985
                                                                                                                                                                                                                                              Mannheimia.
                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                        Pasteurella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00330; HEMOLYSIN_CALCIUM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U01215; AAB36689.1; -
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                                                                                                                                                                                                                                                                                                                                   Leukotoxin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  774 NDLLHGGKGDDI 785
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SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INVOLVED IN PORE FORMATION BY PTM: PALMITOYLATED BY LKTC. TH
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DOMAIN: THE THREE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PR00313; CABNDNGRPT PR01488; RTXTOXINA.
                                                                                                                                                                                                                                                                                                                            6 (Rel. : 6 (Rel. : 0 (Rel. : 1 from se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING , WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
                                                                                                                                                                                                                                                                                        haemolytica
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                                                                                                                                                                                                                                                                                                                               serotype
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                                                                                                                                                                                                                                                                                                                                 34, Last sequence update)
39, Last annotation update)
erotype T10.
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58.3%;
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D BY LKTC. THE TOXIN ONLY BECOMES ACTIVE WHEN
                                                                                                                                                                                                                                                                  gamma
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POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 49; DB Pred. No. 1.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        554321
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6 X REPEATS,
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                                                                                                                                                                                                                                                                  subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 927FF56CFC884F12 CRC64;
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Best Local S
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane; L
Transmem 299
Transmem 361
Transmem 383
DOMAIN 736
REPEAT 745
REPEAT 745
REPEAT 763
REPEAT 763
REPEAT 772
REPEAT 772
REPEAT 781
SEQUENCE 955 A
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SEQUENCE
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between
SEQUENCE FROM N.A.
STRAIN-S 4074 / SEROTYPE 1;
MEDLINE-91348845; PubMed-1879928;
Frey J., Meier R., Gygi D., Nicol.
"Nucleotide sequence of the hemol
pleuropneumoniae.";
                                                                                                                                                                                                                                              ACTPL
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InterPro; IPR003355; RTX_N.
InterPro; IPR003959; RtxA.
Pfam; PF00353; hemolysinCabind; 1.
pfam; PF02382; RTX; 1.
PRINTS; PR00313; CABNDUGRPT.
PRINTS; PR01488; RTXTOXINA.
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                                                                                         Actinobacillus.
NCBI_TaxID=715;
                                                                                                                 Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae) Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00330; HEMOLYSIN_CALCIUM; 4. Hemolysis; Toxin; Cytolysis; Cytotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; 226247; CAA81206.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVE INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIM PTM: PALMITOYLATED BY LKTC. THE TOXIN ONLY BECOMES MODIFIED (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Secreted.

DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                    Similarity 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                    Conservative
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POTENTIAL.
POTENTIAL.
              hemolysin
                            Nicolet
                                                                                                                                                                                                                                                                                                                                                    Score 49; DB
Pred. No. 1.4;
3; Mismatches
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6 X REPEATS,
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              gene
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                                                                                                                                                                   (APX-IA) (Hemolysin
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                Actinobacillus
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STRAIN-S 4074 / SEROTYPE 1;
Chang Y., Wang Y., Chin N.;
Chang Y., Chin N.;
Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases.
FUNCTION: ONE OF THE VIRULENCE FACTORS OF A.PLEUROPN
WHICH HAS A STRONG HEMOLYTIC ACTIVITY AND IS CYTOTOX
ALVEDOLAR MACROPHAGES AND NEUTROPHILS.

-I- SUBCELLULAR LOCATION: Secreted.

-I- SUBCELLULAR LOCATION: Secreted.

-I- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
STRAIN=S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-ISOLATE CVI 13261 / SEROTYPE 9;
MEDLINE-93366425; PubMed-8359891;
Jansen R., Briaire J., Kamp E.M., Gielkens
"Structural analysis of the Actinobacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene 142:97-102(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Infect.
[2]
                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Frey J., Haldimann A., Nicolet J., Boffini A., Prentki P.; "Sequence analysis and transcription of the apxI operon (hemolysin from Actinobacillus pleuropneumoniae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=S 4074 / SEROTYPE MEDLINE=94237497; PubMed=
                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                               DOMAIN
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                                                                                                                                         TRANSMEM
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Hemolysis; Toxin; Cytolysis; Cytotox
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                                                                                                     REPEAT
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                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                 send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MISCELLANDOUS: APXIA IS PARTIALLY DELETED IN SEROTYPES 2
8, 12, AND TOTALLY DELETED IN SEROTYPE 3.
MISCELLANDOUS: THE SEQUENCE SHOWN IS THAT OF SEROTYPE 1.
SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE INVOLVED IN PORE FORMATION BY THE CYTOTOXIN PTM: PALMITOYLATED BY APXIC. THE TOXIN ONLY
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                                                                                                                                                                                                                                                                                      X68595; CAA48586.1;
X73117; CAA51548.1;
U05042; AAB05034.1;
                                                                                                                                                                                                                            PF00353; hemolysinCabind;
PF02382; RTX; 1.
                                                                                                                                                                                                                                                                                                                            X52899; CAA37081.1; -.
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4074
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                                                                                                                                                                  Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=8181764;
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406
406
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                                                                                                                                                                Palmitate.
                                                                                                                POTENTIAL.
POTENTIAL.
13 X REPEA
                                                                                                                                                                            CALCIUM; 2.
Cytotoxin;
      98.765.432.
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                                                                                                                                                                                                                                                                                                                                                                                                      There are no
                                                                                                                                                                               Repeat;
                                                                                                                                                                                                                                                                                                                                                                                         as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.L.J., Smits M.A.; pleuropneumoniae-RTX-toxin
                                                                                                                    GLY-RICH
                                                                                                                                                                                                                                                                                                                                                                            Usage
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Y BECOMES ACTIVE V
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nagai S., Yagihashi T., Ishihama A.; "DNA sequence analysis of an allelic pleuropneumoniae RTX-toxin I (ApxIA) Microb. Pathog. 15:485-495(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=K17 / SEROI
                                                                                                                                                                                                                                                                                                                                                                                                                                               Chin N., Frey J., Chang C.F., Chang "Identification of a locus involved Actinobacillus pleuropneumoniae."; FEMS Microbiol. Lett. 143:1-6(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=13039 / SEROTYPE 10;
MEDLINE=94276858; PubMed=8007819;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Actinobacillus pleuropneumoniae Bacteria; Proteobacteria; gamma Actinobacillus.
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01-OCT-1996
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P55129;
                                                                                                                                                                          MEDLINE=93366425; PubMed=8359891;
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 886-1023 FROM N.A. STRAIN-K17 / SEROTYPE 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=K17 / SEROTYPE 5;
MEDLINE=96401417; PubMed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=715;
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                                                                                                                                                                                                                                                                                                                             Jansen R., Briaire J., Kamp E.M., Gielkens "Structural analysis of the Actinobacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FNDIFHSGEGDD
MISCELLANEOUS: APXIA IS PARTIALLY DELETED 8, 12, AND TOTALLY DELETED IN SEROTYPE 3. MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT SIMILARITY: BELONGS TO THE RTX PROKARYOTIC
                                                                            DOMAIN: THE THREE TRANSMEMBRANE D
INVOLVED IN PORE FORMATION BY THE
PTM: PALMITOYLATED BY APXIC: THE
MODIFIED (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=8807793;
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Pred. No.
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R -> A (IN REF. 3 AND 4).
Q -> E (IN REF. 3 AND 4).
TC -> R (IN REF. 3 AND 4).
TC -> R (IN REF. 3 AND 4).
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        RTX PROKARYOTIC TOXIN FAMILY.
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in the
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pes 5/10
                                                                                                     E CYTOTOXIN
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                        THAT OF SEROTYPE
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Pasteurellaceae;
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                                                                                                     BELIEVED TO BE (BY SIMILARITY).
                                                                SEROTYPES
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InterPro; IPR003355; RTX_N.
InterPro; IPR003995; RtxA.
Pfam; PP00353; hemolysinCabind; 2.
Pfam; PF00352; RTX; 1.
Pfam; PF02382; RTX; 1.
PRINTS; PR01313; CABNDUGRPT.
PRINTS; PR01313; CABNDUGRPT.
PRINTS; PR01313; PR01481; CYTONINA.
PROSITE; PS00330; HEMOLYSIN_CALCIUM; 2.
Hemolysis; Toxin; Cytolysis; Cytotoxin; Re
                                                                                        HLY1_ECOLI
P09983;
01-MAR-1989
01-MAR-1989
30-MAY-2000
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SEQUENCE
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SEQUENCE FROM N.A.
STRAIN-J96 / SEROTYPE 04;
MEDLINE-85234404; PubMed-3891743;
Felmlee T., Pellett S., Welch R.A.;
                                                         Escherichia
Bacteria; P
                                                                                                                                                                                                                                                                                      REPEAT
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                                                                                Hemolysin,
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                                                  Escherichia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long
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                                         NCBI_TaxID=562;
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; U04954;
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                                                                                                                                                                                                      Similarity
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                                                                                 chromosomal.
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(Rel. 10, Last sequence update)
(Rel. 39, Last annotation update)
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26 256
27 326
37 406
57 406
22 845
22 727
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                                                         subdivision; Enterobacteriaceae;
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    Q (IN REF. 2).
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    L (IN REF. 2).
    183C7C15EE57DB55 CRC64;

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InterPro; IPR001343; Hemlysn_Ca
InterPro; IPR003355; RTX_N.
InterPro; IPR003995; RtxA.
Pfam; PF00353; hemolysinCabind;
Pfam; PF02382; RTX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Characterisation of HlyC and mechanism of haemolysin from E. coli 2001."; FEBS Lett. 187:339-344(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Nucleotide sequence of an Escherichia coli chromosomal hemolysin.";
J. Bacteriol. 163:94-105(1985).
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SEQUENCE OF 1-44 FROM N.A.
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                                                                                                                                                                                                                                                         Transmembrane;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MODIFIED.

DISEASE: THE HEMOLYSIN OF E.COLI IS PRODUCED PREDOMINANTLY STRAINS CAUSING EXTRAINTESTINAL INFECTIONS, SUCH AS THOSE CURINARY TRACT.
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A -> T (IN STRAIN 2001).
A -> T (STRAIN 2001).
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POTENTIAL.
16 X REPEA
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X MEDILINE=90078125; pubMed=2687250;

A de Maagdd R.A., Wijfjes A.H.M., Spaink H.P., Ruiz-Sainz J.E.,

A de Maagdd R.A., Wijfjes A.H.M., Spaink H.P., Ruiz-Sainz J.E.,

A Wijffelman C.A., Okker R.J.H., Lugtenberg B.J.J.;

I nodO, a new nod gene of the Rhizobium leguminosarum biovar viciae

I sym plasmid pRIJJI, encodes a secreted protein.";

I J. Bacteriol. 171:6764-6770(1989).

I J. Bacteriol. 171:6764-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _RHILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The Rhizobium nodulation W.D.O., Johnston A.W.B., Downie J.A.;
"The Rhizobium nodulation gene nodO encodes a Ca2(+)-binding protein that is exported without N-terminal cleavage and is homologous to haemolysin and related proteins.";
EMBOL TO ANALYSIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rhizobium leguminosarum (biovar viciae).
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                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X17285; CAA35178.1;
EMBL; M29532; AAA26341.1;
PIR; S08385; S08385.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBO J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=90151607;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria;
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          SEQUENCE
                                                                                                                                                                                                                                 PRINTS; PR00313; CABNUNGRPT PROSITE; PS00330; HEMOLYSIN_
                                                                                                                                                                                                                                                                                                                                                                                                PIR; A43721; A43721.
                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                InterPro; IPR001343; Hemlysn_Ca_bind
InterPro; IPR003355; RTX_N.
                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                   Plasmid;
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                                                                                                                                                                                                                                                                                                  PF00353; hemolysinCabind; 2.
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8; Conser
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                                                                                                                                                                                                                                     HEMOLYSIN_CALCIUM; 1.
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8 X APPROXIMATE T
4 X APPROXIMATE T
POTENTIAL.
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S OR SOME OTHER PLA
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REPEATS,

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7.5.4.3.1

DOMAIN TRANSMEM TRANSMEM Transmembrane; Hemolysis; Toxin;

TRANSMEM

238

Lipoprotein;

Cytolysis; HEMOLYSIN\_CALCIUM;

Cytotoxin; Palmitate. POTENTIAL. POTENTIAL.
9 X REPEAT

Repeat; Calcium;

PROSITE; PS00330;

PRINTS; PRINTS;

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01-APR-1993 (Rel. 25, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Hemolysin (Cytolysin II) (CLY-IIA) (HLY-IIA)
APPA OR CLYIIA OR HLYIIA OR CYTC.
                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed. Usage humor sequires a license agreement.
                                                                                                                                                              InterPro; IPR003995; RtxA.
pfam; pF00353; hemolysinCabind;
pfam; pF02382; RTX; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=92267623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-3714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Actinobacillus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Actinobacillus suis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q00951;
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InterPro; IPR003355;
                                                                                                                                                                                                                 EMBL; M90440; AAA21918.1;
                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: Secret
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=1587585;
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                                                                                                                                                                                                        Hemlysn_Ca_bind.
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                       InterPro;
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01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation updat
RTX-II toxin determinant A (APX-IIA) (Hemol
                                                                                      PIR;
PIR;
                                                                                                                                                                                                                                             the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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STRAIN-SEROTYPE 5;
MEDLINE-90126233; PubMed-2693022;
Chang Y.-F., Young R., Struck D.K.;
"Cloning and characterization of a hemolysin gene (Haemophilus) pleuropneumoniae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Actinobacillus pleuropneumoniae Bacteria; Proteobacteria; gamma Actinobacillus.
                                                                                                                                                                                                                               entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gielkens A.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-ISOLATE CVI 13261 / SEROTYPE MEDLINE-92040145; PubMed-1937809;
                                                                                                                                   EMBL; M30602; AAA87232.1;
EMBL; X61111; CAA43423.1;
                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Smits M.A., Briaire
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Cytolysin IIA) (CLY-IIA).
APXIIA OR CLYIIA OR HLYIIA OR APPA OR CYTC.
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                                                                                                                                                                                                                                                                                                                        between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=715;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Cytolysins of Actinobacillus pleuropneumoniae Infect. Immun. 59:4497-4504(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              731
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DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING

CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLI

CACTIVITY (BY SIMILARITY)

DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE
INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY)

PTM: PALMITOXLATED BY AFXIIC. THE TOXIN ONLY BECOMES ACTIVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: ONE OF THE VIRULENCE FACTORS OF WHICH SHOWS A WEAK HEMOLYTIC ACTIVITY AND FOR ALVEOLAR MACROPHAGES AND NEUTROPHILS.
                  SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                             MODIFIED (BY SIMILARITY)
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  hemolysinCabind; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      update)
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Pasteurellaceae;
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IS MODERATELY CYTOTOXIC
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RESULT 18
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SEQUENCE
                                                                                           use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-93239320; PubMed-8478098;
Chang Y.-F., Ma D.-P., Shi J., Chengappa M.M.;
"Molecular characterization of a leukotoxin ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPEAT
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   InterPro;
                                EMBL; L12148; AAA16444.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pasteurella haemolytica-like sp. (strain 5943B).
Bacteria; Proteobacteria; gamma subdivision; Pas
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30-MAY-2000
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                                                                                                                                                                                                                       European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                            ACTIVITY.

DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY). PTM: PALMITOYLATED BY LATC. THE TOXIN ONLY BECOMES ACTIVE WHEN MODIFIED (BY SIMILARITY).

SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sct. Immun. 61:2089-2095(1993).
FUNCTION: VIRULENCE FACTOR WHICH
IS NOT HEMOLYTIC.
                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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7; Conserv
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(Rel. 34, Last sequence up
(Rel. 39, Last annotation
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Pred. No.
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                                                                                                                     . Usage by and for commercial http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                        RX MEDLINE-96011363; PubMed-7592325;
RA WASSIF C., Cheek D., Belas R.;
RA WASSIF C., Cheek D., Belas R.;
RI "Molecular analysis of a metalloprotease from Proteus mirabilis.";
RI J. Bacteriol 177.5790-5798(1995).
GC C.;
FUNCTION: ONE OF THE VIRULENCE FACTORS PRODUCED DURING SWARMER
CC -:- FUNCTION: ONE OF THE BACTERIA, WHICH SEEMS TO BE ASSOCIATED
CC CICLL DIFFERENTIATION OF THE BACTERIA, WHICH SEEMS TO BE ASSOCIATED
CC IG A2, AS WELL AS IG G DEGRADATION.
CC IG A2, AS WELL AS IG G DEGRADATION.
CC -:- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
CC -:- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
CC -:- ENZYME REGULATION: CA2+ INCREASES PROTEASE ACTIVITY.
C-:- ENZYME REGULATION: CA2+ INCREASES PROTEASE ACTIVITY.
CC -:- SUBCELLULAR LOCATION: Secreted.
C-:- SUBCELLULAR SECRETION OF THIS METALLOPROTEASE.
C-:- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M10B (ZINC
METALLOPROTEASE); ALSO KNOWN AS THE SERRALYSIN SUBFAMILY.
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01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
01-0CT-1996 (Rel. 34, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF02382;
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InterPro; IPR003995;
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                                                 use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria;
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ne; Lipoprotein; Palmitate.
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312 333 POTENTIAL.
393 414 POTENTIAL.
325 780 7 X REPEATS, G.
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30 74 3.
19 744 3.
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          AAA86729.1;
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          ALT_INIT
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Pred. No. 6.9;
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7 X REPEATS, GLY-RICH
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                                                                                  (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Repeat; Calcium;
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MEROPS; M10.057; -.

InterPro; IPR001343; Hemlysn_Ca_bind.

InterPro; IPR00130; Zn_MTpeptdse.

Pfam; PF00353; hemolysinCabind; 1.

PRINTS; PR00313; CABMONGRPT.

SMART; SM00235; ZnMC; 1.
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347 NDIIHGNDADNTLIGGEGDDII 368
                                                   2 NDIFH-----
                                                                                                 l Similarity
9; Conserv
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Pred. No. 8
                                                                                                                                                                                                                                                                                                                                                                                                               ZINC
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BY SIMILARITY.
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(CATALYTIC)
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(BY SIMILARITY).
(BY SIMILARITY).
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Search completed: September 11, job time: 278 sec 2002, 09:01:55

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Result
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                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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hypothetical prote probable secreted probable outer mem conserved hypothet probable protein k hypothetical prote iron-regulated procalcium-binding pr
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hypothetical prote
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### ALIGNMENTS

A;Status: nucleic acid sequence not shown; not compared with conceptual translation A;Molecule type: DNA A;Residues: 430-438, 'S',440-476, 'R',478-506, 'RVRS',511, 'QSIAINSLNTD',523-541,'I',543, A;Note: this sequence is revised in reference A34345 R;Ohta, H; Miyagi, A.; Kato, K.; Fukui, K. submitted to JIPID, July 1995 submitted to JIPID, July 1995 A;Description: Modulation of leukotoxin production by growth rate and bicarbonate in A;Reference number: PH0266 A;Accession: PH0266 A;Accession: PH0267 A;Molecule type: protein A;Residues: 17-42 <ohts 301-b="" a;accession:="" a;experimental="" ph0266<="" source:="" strain="" td=""><td>A;Accession: B34345 A;Molecule type: DNA A;Molecule</td><td>sing nucleotide R;Kolodrubetz, D.; Dailey, T.; Ebersole, J.; Kraig, E. Infect. Immun. 57, 1465-1469, 1989 A;Title: Cloning and expression of the leukotoxin gene from Actinobacillus actinomyc- A;Reference number: A60768; MUID:89212893 A;Accession: A60768 A;Status: nucleic acid sequence not shown; not compared with conceptual translation A;Status: nucleic acid sequence not shown; not compared with conceptual translation A;Coule type: DNA A;Residues: 297-309,'Y',311-364;434-440,'KC',443-474,'H',476-489,'S',491-493,'VLK',49 A;Note: this sequence is revised in reference A37205 R;Lally, E.T.; Golub, E.E.; Kieba, I.R.; Taichman, N.S.; Rosenbloom, J.; Rosenbloom, Biol. Chem. 264, 15451-15456, 1989 J;Title: Analysis of the Actinobacillus actinomycetemcomitans leukotoxin gene. Deline A;Reference number: A34345; MUID:89359382</td><td>RESULT 1 A37205 A37205 Leukotoxin A - Actinobacillus actinomycetemcomitans C;Specles: Actinobacillus actinomycetemcomitans C;Date: 16-Sep-1992 #sequence_revision 01-Nov-1996 #text_change 31-Mar-2000 C;Accession: A37205; A60768; B34345; A32276; PH0267; PH0266; S17284 R;Kratg, E; Dailey, T.; Kolodrubetz, D. Infect. Immun. 58, 920-929, 1990 A;Title: Nucleotide sequence of the leukotoxin gene from Actinobacillus actinomycetem A;Reference number: A37205; MUID:90202154 A;Accession: A37205 A;Accession: A37205 A;Cross-references: GB:X16829; NID:g38643; PIDN:CAA34731.1; PID:g38645 A;Cross-references: GB:X16829; NID:g38643; PIDN:CAA34731.1; PID:g38645 A;Note: the authors present evidence that the nucleotide sequence is correct in the v</td></ohts>	A;Accession: B34345 A;Molecule type: DNA A;Molecule	sing nucleotide R;Kolodrubetz, D.; Dailey, T.; Ebersole, J.; Kraig, E. Infect. Immun. 57, 1465-1469, 1989 A;Title: Cloning and expression of the leukotoxin gene from Actinobacillus actinomyc- A;Reference number: A60768; MUID:89212893 A;Accession: A60768 A;Status: nucleic acid sequence not shown; not compared with conceptual translation A;Status: nucleic acid sequence not shown; not compared with conceptual translation A;Coule type: DNA A;Residues: 297-309,'Y',311-364;434-440,'KC',443-474,'H',476-489,'S',491-493,'VLK',49 A;Note: this sequence is revised in reference A37205 R;Lally, E.T.; Golub, E.E.; Kieba, I.R.; Taichman, N.S.; Rosenbloom, J.; Rosenbloom, Biol. Chem. 264, 15451-15456, 1989 J;Title: Analysis of the Actinobacillus actinomycetemcomitans leukotoxin gene. Deline A;Reference number: A34345; MUID:89359382	RESULT 1 A37205 A37205 Leukotoxin A - Actinobacillus actinomycetemcomitans C;Specles: Actinobacillus actinomycetemcomitans C;Date: 16-Sep-1992 #sequence_revision 01-Nov-1996 #text_change 31-Mar-2000 C;Accession: A37205; A60768; B34345; A32276; PH0267; PH0266; S17284 R;Kratg, E; Dailey, T.; Kolodrubetz, D. Infect. Immun. 58, 920-929, 1990 A;Title: Nucleotide sequence of the leukotoxin gene from Actinobacillus actinomycetem A;Reference number: A37205; MUID:90202154 A;Accession: A37205 A;Accession: A37205 A;Cross-references: GB:X16829; NID:g38643; PIDN:CAA34731.1; PID:g38645 A;Cross-references: GB:X16829; NID:g38643; PIDN:CAA34731.1; PID:g38645 A;Note: the authors present evidence that the nucleotide sequence is correct in the v

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A; Molecule type: protein
A; Residues: 2-6, 'L', 8-26 <
C; Genetics:
A; Gene: ltxA
C; Function: lyses human
A; Description: lyses human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: apxIIIA
C;Function:
C;Function: lyses lung macrophages
A;Description: lyses lung macrophages
C;Superfamily: hemolysin A; hemolysin A homology
C;Keywords: calcium binding; cytolysis; exotoxin; lipoprotein; tap;254-803/Domain: hemolysin A homology <HLYA>
F;733-861/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIYF]-X)
F;571,702/Binding site: palmitate (Lys) (covalent) #status predic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Description: lyses human polymorphonuclear lymphocytes and monocytes C;Superfamily: hemolysin A; hemolysin A homology C;Keywords: cytolysis; hemolysis; lipoprotein; periplasmic space; tandem F;245-790/Domain: hemolysin A homology <HLYA>
F;731-847/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIYF]-X) F;562,687/Binding site: palmitate (Lys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-1049 <CHA>
A; Cross-references: EMBL:L12145; NID:g349605; PIDN:AAA21924.1;
C; Comment: This orgnism causes porcine pleuropneumonia.
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: S51784
R;Chang, Y.F; Shi, J.; Ma, D.P.; Shin, S.J.; Lein, D.H.
DNA Cell Biol. 12, 351-362, 1993
A;Title: Molecular analysis of the Actinobacillus pleuropneumoniae
A;Reference number: S51783; MUID:93263992
A;Accession: S51784
                                                                                                                                                   toxin III - Actinobacillus pleuropneumoniae (serotype 8)
N;Alternate names: RTX-toxin III (ApxIIIA)
C;Species: Actinobacillus pleuropneumoniae
C;Date: 19-Dec-1993 #sequence_revision 01-Nov-1996 #text_change 18-Jun-1999
C;Accession: B49219; S48043; S29958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      toxin III - Actinobacillus pleuropneumoniae (serotype N;Alternate names: RTX-toxin IIIA (ApxIIIA) C;Species: Actinobacillus pleuropneumoniae C;Date: 14-Jul-1995 #sequence_revision 15-Nov-1996 #te
                                           A; Title: Cloning and characterization of the A; Reference number: A49219; MUID:93162836 A; Accession: B49219
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A; Molecule type: DNA
A; Residues: 1-1052 < JAN1>
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                                                                                                            n, R.; Briaire, J.; Kamp, E.M.; Gielkens, A.L.; Immun. 61, 947-954, 1993
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64.3%;
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Pred.
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Pred. No. 0.088;
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                                                                                         Actinobacillus pleuropneumoniae-RTX-toxin
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hemolysin - Escherichia coli C;Species: Escherichia coli C;Date: 31-May-1996 #sequence\_revision ^.^^assion: I41078

31-May-1996

#text\_change

21-Jul-2000

**I41078** 

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..., LTLE: Nucleotide sequence of A; Reference number: $07209
A; Accession: $10056
A; Status: prel:-
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A; Note: sequence extracted from NCBI backbone (NCBIN:125168, NCBIP:125170)
R; Jansen, R.; Briaire, J.; van Geel, A.B.M.; Kamp, E.M.; Gielkens, A.L.J.;
Infect. Immun. 62, 4411-4418, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Description: lyses lung macrophages (C;Superfamily: hemolysin A; hemolysin A homology C;Superfamily: hemolysin A; hemolysis; exotoxin; lipoprotein; t F;254-804/Domain: hemolysin A homology cHLYA>
F;736-862/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIYF]-X)
F;571,702/Binding site: palmitate (Lys) (covalent) #status predi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Genetic map of the Actinobacillus pleuropneumoniae RTX-toxin (Apx) operons: A;Reference number: $48042; MUID:95012630 A;Recession: $4804 Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                A;Genome: plasmid pH1y152
C;Superfamily: hemolysin A; hemolysin A homology
C;Keywords: lipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Escherichia coli
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997
C;Accession: S10056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Function:
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A;Experimental source: strain 405, serotype 8
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, Ju
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A; Residues: 1-1024 <HES>
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RESULT
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A;Residues: 1-1052 <JAN2>
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9; Conser
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71.4%;
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Pred. No. 0.13
1; Mismatches
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R;Schmidt, H.; Beutin, L.; Karch, Infect. Immun. 63, 1055-1061, 199

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A; Status; preliminary; translated from GB/EMBL/DDB
A; Status; preliminary; translated from GB/EMBL/DDB
A; Molecule type: DNA
A; Residues: 1-998 <BUR>
A; Cross-references: EMBL:AF074613; PIDN:AAC70116.1
A; Experimental source: strain EDL933; serotype O15
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A;Title: Complete nucleotide sequences of neference number: Z14127; MUID:98290540
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A;Accession: I41078
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-998 <RES>
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C;Superfamily: hemolysin A; hemolysin A homology
C;Keywords: cytolysis; hemolysis; lipoprotein; to
F;233-776/Domain: hemolysin A homology <HLYA>
F;550,675/Binding site: palmitate (Lys) (covalent
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hypothetical protein all2655 C; Species: Anabaena sp.
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A; Accession: T00227
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57.1%;
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57.1%;
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Pred. No. 1.3;
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N;Alternate names: lktA protein
C;Species: Pasteurella haemolytica (fragment)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan 06;Accession: S34238; S34732
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A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubl
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.
L.; Hyman, R.W.; Jones, T.
Science 293, 568-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelau
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelau
A;Authors: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
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R; Finan, T.M.; Weldner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A; Title: The complete sequence of the 1,683-kb pSymB megaplasmid A; Reference number: A95842; MUID:21396508; PMID:11481431
A; Accession: E95995
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A;Molecule type: DNA
A;Residues: 1-3262 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB74354.1; PID:g17131748; GSPDB:GN00179
A;Cross-references: strain PCC 7120
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A; Residues: 1-387 <KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F.J.;
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06-Jan-1995 #text\_change

23-Mar-2001

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A; Description: lyses leukocytes C; Superfamily: hemolysin A; hemolysin A homology C; Keywords: calcium binding; cytolysis; exotoxin; hemolysis; lipo F; 238-784/Domain: hemolysin A homology HLYA>
F;716-807/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIYF]-X)
F;554/Binding site: palmitate (Lys) (covalent) #status predicted
                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-741,'D',743-953 <LOR>
A; Residues: 1-741,'D',743-953 <LOR>
A; Cross-references: EMBL: M20730; NID: g150492; PIDN: AAA25529.1; PID: g150494
C; Comment: This organism causes bovine pneumonic pasteurellosis (shipping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Pasteurella haemolytica
C;Date: 12-Oct-1989 #sequence_revision 15-Nov-1996 #text_change 18-Jun-1999
C;Accession: B30169; C32051; S29516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
B30169
                                                                                                                                                                           C; Function:
                                                                                                                                                                                                A; Gene:
                                                                                                                                                                                                                         C; Genetics:
                                                                                                                                                                                                                                                                                                                                  A; Title: Nucleotide sequence of the leukotoxin A; Reference number: S29515; MUID:87306837 A; Accession: S29516
                                                                                                                                                                                                                                                                                                                                                                                              R;Lo, R.Y.C.; Strathdee, C.A.; She Infect. Immun. 55, 1987-1996, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-953 <HIG>
R;Strathdee, C.A; Lo, R.Y.C.
R. Bacteriol. 171, 916-928, 1989
A;Title: Cloning, nucleotide sequence, and A;Reference number: A32051; MUID:89123172
A;Accession: C32051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Title: DNA sequence of the Pasteurella haemolytica leukotoxin gene cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Highlander, S.K.
DNA 8, 15-28, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N; Alternate names: lktA
C; Species: Pasteurella h
C; Date: 12-Oct-1989 #seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:Z22886; NID:g311826; PIDN:CAA80500.1; A;Experimental source: serotype T15 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 9-208 <LA2>
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A;Experimental source: serotype
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A; Residues: 1-208 <LAI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 947-953 <STR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: not compared with conceptual translation
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A;Accession: S34238
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Best Local
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58.3%;
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T4
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Pred. No.
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C;Function:
A;Description: attacks cell membranes ....
C;Superfamily: hemolysin A; hemolysin A homology
C;Superfamily: hemolysin A; hemolysis; exotoxin; hemolysis; lipo
C;Keywords: calcium binding; cytolysis; exotoxin; hemolysis; lipo
cytolysis; exotoxin; hemolysin A homology cytoxin; hemolysis; lipo
cytoxidae, calcium binding; exotoxin; hemolysis; lipo
cytoxidae, calcium binding; cytoxidae, cytox
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 745-955 <LA2>
A;Cross-references: EMBL:Z22884; NID:g311828; PIDN:CAA80498.1;
A;Experimental source: serotype T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Description: DNA sequence of the carboxy terminal A;Reference number: $34235 A;Accession: $34237
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A;Molecule type: DNA
A;Residues: 950-955 <HIG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:Z26247; NID:g400424; PIDN:CAA81206.1; R;Highlander, S.K.; Engler, M.J.; Weinstock, G.M. J. Bacteriol. 172, 2343-2350, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Description: DNA sequence of the leukotoxin A;Reference number: S37145 A;Accession: S37145
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A; Residues: 723-955 <LA3>
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                                                                                                                                                                                                                                                          F;801-809/Region:
                                                                                                                                                                                                                                                                                     F;792-800/Region:
                                                                                                                                                                                                                                                                                                                                                                F;772-780/Region:
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A; Residues: 1-955 <LAI>
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                                                                Matches
                                                                                              Query Match
Best Local
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   NDIFHSGEGDDL
                                                                Similarity 7; Conserv
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                                                                Conservative
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13
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58.3%;
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                                                                                           Score 49;
Pred. No.
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Pred. No.
                                                            Mismatches
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A; Molecule type: DNA
A; Residues: 604-685 <TAS>
A; Residues: 604-685 <TAS>
C; Comment: This organism causes porcine pleuropneumonia.
C; Genetics:
A; Genetics:
A
signal-transducing histidine kinase homolog - Archaeoglobus fulgidus C.Species: Archaeoglobus fulgidus C.Species: Archaeoglobus fulgidus C.Species: O5-Dec-1997 #sequence_revision O5-Dec-1997 #text_change O2-Sep-2000 C.Accession: E69361
R.Klenk, H.P., Clayton, R.A.: Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, F.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.: Sutton C.C.: City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Infect. Immun. 61, 3688-3695, 1993
A.Title: Structural analysis of the Actinobacillus pleuropneumoniae-RTX-toxin I (ApxI)
A;Reference number: I39641; MUID:93366425
A;Accession: I39643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Frey, J.; Haldimann, A.; Nicolet, J.; Boffini, A.; Prentki, Gene 142, 97-102, 1994
A;Title: Sequence analysis and transcription of the apxI operch; R;Feference number: 139644; MUID:94237497
A;Accession: 139645
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C;Species: Actinobacillus pleuropneumoniae
C;Species: Actinobacillus pleuropneumoniae
C;Date: 19-Jul-1996 #sequence_revision 08-Nov-1996 #text_change 18-Jun-1999
C;Accession: I39643; S18769; I39645; S60732; S35781
C;Accession: R;Briaire, J; Kamp, E.M.; Gielkens, A.L.; Smits, M.A.
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A; Residues: 1-209, 'AMPYLTLA', 218-373, 'R', 375-561, 'Q', 563-686, 'TC', 688-1022 <RE2>
A; Cross-references: EMBL: X68595; NID: g505568; PIDN: CAA48586.1; PID: g505570
A; Cross-references: EMBL: X68595; AID: g505568; PIDN: CAA48586.1; PID: g505570
R; Tascon, R.I.; Vazquez-Boland, J.A.; Gutierrez-Martin, C.B.; Rodriguez-Barbosa,
Mol. Microbiol. 14, 207-216, 1994
Mol. Microbiol. 14, 207-216, 1994
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A; Cross-references: EMBL:X73117; NID:g312897; R; Frey, J.; Meier, R.; Gygi, D.; Nicolet, J. Infect. Immun. 59, 3026-3032, 1991
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A;Accession: S60732
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A; Residues: 1-209, 'AMPYLTLA', 218-373, 'R', 375-561, 'Q', 563-686, 'TC', 688-1022
A; Cross-references: EMBL: X52899; NID: 938949; PIDN: CAA37081.1; PID: 938950
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A;Accession: S18769
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Pred. No. 4
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    F.; White, O.; Nelson, K.E.; Ketchum, K.A.; D
Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness,
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A; Description: attacks blood cell membranes and causes cell lysi: C; Superfamily: hemolysin A; hemolysin A homology C; Keywords: calcium binding; cytolysis; exotoxin; hemolysis; lip: F; 246-791/Domain: hemolysin A homology <HLYA> .
F; 723-851/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIYF]-X) F; 563,689/Binding site: palmitate (Lys) (covalent) #status exper
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A; Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Smith, H.O.; Woese, C.R.; Venter, J.C.
A; Title: The complete genome sequence of the hyperthe A; Reference number: A69250; MUID:98049343
A; Accession: E69361
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A;Residues: 1-1023 <FEL>
A;Cross-references: GB:M10133; GB:M12863; NID:g146377;
A;Experimental source: strain J96, O4 serotype
A;Experimental source: Koronakis, V.; Hughes, C.
Science 266, 1992-1996, 1994
Science 266, 1992-1996, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Felmlee, T.; Pellett, S.; Welch, R.A.
J. Bacteriol. 113, 94-105, 1985
A;Title: Nucleotide sequence of an Escherichia
A;Reference number: A24433; MUID:85234404
A;Accession: A24433
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Best Local Similarity
"---hes 9; Conserv
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A;Residues: 1,'T',3,'Y',5,'T',7-44 <RES>
A;Cross-references: GB:M29173; NID:g146337; PIDN:AAA23957.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Fatty acylation of two internal lysine residues required A;Reference number: A55387; MUID:95099325
A;Contents: annotation; lysine paimitoylation A;Note: lysine modification is performed by the hlyC gene product R;Haertlein, M.; Schiessi, S.; Wagner, W.; Rdest, U.; Kreft, J.; G J. Cell Biol. 22, 87-97, 1983
A;Title: Transport of hemolysin by Escherichia coli.
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A; Residues: 1-334 <KLE>
                                                                                                                                                                                                                                                                                                       C; Function
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A; Accession: I41280
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Best Local
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69.2%;
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66.7%;
                                             Score 48; DB Pred. No. 6.3; Nismatches
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Pred. No. 1.8;
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                                                                                        Length 1023;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIDN:AAA23975.1; PID:g146379
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                                                                                                                                                                                                                                                                                                                                                                          PID:g146338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J.; Goebel,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for
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hypothetical protein all7655 [imported] - Anabaena sp. (strain PCC 7120) plasmid pCC712d C;Species: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120 A;Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002 C;Accession: AD2546 C;Accession: AD2546 C;Accession: AD2546 C;Accession: AC;Simpo, S.; Sugimoto, M.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, Sunkazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, Sunkazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, Sunkazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, Sunkazawa, M.; Yasuda, M.; Yasuda, M.; Tabata, Sunkazawa, M.; Yasuda, M.; Yasuda, M.; Tabata, Sunkazawa, M.; Yasuda, M.; Tabata, Sunkazawa, M.; Yasuda, M.; Yasu
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Search completed: September 11, 2002, 09:00:14 Job time: 232 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 61.0%;
Best Local Similarity 75.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                     3 DIFHSGEGDDLL 14
|||| | ||||
85 DIFHRGGADDLL 96
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Title:
Perfect score:
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                       Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Issued_Patents_AA:*
1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
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               US-09-884-696-13
77
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11.146 Million cell updates/sec
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Comp
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/ABCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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              DB
                                                  US-08-772-270A-11
PCT-US93-1D500-2
US-08-258-188-2
US-08-526-813-2
PCT-US95-08554-2
US-08-619-812-8
US-07-908-253-2
US-08-694-665-6
US-08-878-748-6
US-08-878-748-6
US-08-455-970A-12
US-08-455-970A-12
US-08-455-970A-14
US-08-455-970A-14
US-08-455-970A-14
US-08-455-970A-14
US-08-455-970A-14
US-08-455-970A-14
US-08-455-970A-14
US-08-455-970A-14
US-08-455-970A-14
US-08-878-748-8
US-08-878-748-8
US-08-878-748-8
US-08-878-748-8
US-08-878-748-8
US-08-878-748-8
US-08-878-748-8
US-08-777-715-9
US-08-170-126-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Compugen Ltd.
sequence 2, Appl
Sequence 6, Appl
Sequence 6, Appli
Patent No. 5476657
Sequence 10, Appl
Sequence 10, Appl
Sequence 8, Appli
sequence 8, Appli
sequence 8, Appli
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uence 8, Appli
uence 2, Appli
ence 2, Appli
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Sequence
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2 Appli
2 Appli
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3 Appli
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6 Appli
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US-08-772-270A-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11,
           Query Match 75...
Best Local Similarity 71...
Matches 10; Conservative
```

Database

Searched:

Run on:

Result

75.3%; 71.4%;

Score 58; DB Pred. No. 0.11
1; Mismatches

DB 3; 0.11;

Length 1049; Indels

0

Gaps

0

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40	40	40	40	40	40	40	40	40	40	41	41	41	42	42	45	46	49
51.9	51.9	51.9	51.9	51.9	51.9	51.9	51.9	51.9	51.9	53.2	53.2	53.2	54.5	54.5	58.4	59.7	63.6
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US-08-223-305C-48	US-08-455-543A-48	US-08-311-363-13	US-07-745-206A-13	US-08-311-363-15	US-07-745-206A-15	US-09-173-133-10	US-09-173-492-10	US-08-920-440B-10	US-09-609-324A-10	US-08-669-785-4	US-08-387-942C-3	US-08-387-942C-43	5183745-6	US-08-669-785-2	US-08-215-805A-80.	US-08-772-270A-8	US-08-954-418-2
Sequence 48, Appl	Sequence 48, Appl	•	`	Sequence 15, Appl	•	Sequence 10, Appl	•	Sequence 10, Appl	•	Sequence 4, Appli	Sequence 3, Appli	Sequence 43, Appl	Patent No. 5183745	Sequence 2, Appli	Sequence 80, Appl	Sequence 8, Appli	Sequence 2, Appli

### ALIGNMENTS

```
US-08-772-270A-11
                                                                                                                                                                APPLICATION NUMBER: US/08/772,270
FILING DATE: December 23, 1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Gravelle, Micheline
REGISTRATION NUMBER: 40,261
REFERENCE/DOCKET NUMBER: 6580-81
REFERENCE/DOCKET NUMBER: 6580-81
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Actinobacillus pleuropneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: MacInnes, Janet
APPLICANT: Ricciatti, Paul
APPLICANT: Mallard, Bonnie
APPLICANT: Mallard, Bonnie
APPLICANT: Rosendal, Soren
TITLE OF INVENTION: NOVEL BACTERIAL PREPARATIONS, METHOD FOR
TITLE OF INVENTION: PRODUCING SAME, AND THEIR USE AS VACCINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 40 Kin
CITY: Toronto
STATE: Ontario
COUNTRY: Canad
ZIP: M5H 3Y2
                                                                                     LENGTH: 1049 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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                                                                           linear
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RESULT 2 PCT-US93-10500-2

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APPLICANT: Chang, Yung-Fu
             Sequence 2, Application US/08258188 Patent No. 5475098 GENERAL INFORMATION:
                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: KORMAN, Alan S.
REGISTRATION NUMBER: 33,932
REFERENCE/DOCKET NUMBER: 196(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-853-8104
TELEFAX: 716-853-8109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 716-853-8109
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING DATE: 05-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1244 amino acid
TYPE: amino acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                           FRAGMENT TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE:
                                                                                                                               920
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                           ORGANISM: Actinobacillus p
STRAIN: Serotypes 2, 3, 4,
INDIVIDUAL ISOLATE: Swine
CELL TYPE: Gram negative k
                                                                                                                                                                                          Local Similarity nes 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
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                                                                                                                                                            1 FNDIFHSGEGDDLL 14
                                                                                                                             FRDIFHGADGDDLL 933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1244 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                           NO
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                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                          Actinobacillus pleuropneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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NO
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                                                                                                                                                                                                                                                                                           Gram negative bacterium
                                                                                                                                                                                                                                                                                                                                                                          N-terminal
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 Robert H.
                                                                                                                                                                                                             75.3%;
71.4%;
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2
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                                                                                                                                                                                                                                                                                                                           3, 4, 6 and
                                                                                                                                                                                                             Score 58; DB 5
Pred. No. 0.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19603/00001
                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                            DB 5;
                                                                                                                                                                                                                          Length 1244;
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                                                                                                                                                                                                                                                                                      PATENT OF INVENTION: A New and Distinctive DNA Sequence of E. Patent No. 5756293
TITLE OF INVENTION: coli 0157:H7 and its Use for the Rapid, TITLE OF INVENTION: Specific Detection of 0157:H7 and Other TITLE OF INVENTION: E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08526813 Patent No. 5756293 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query-Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415) 543-50 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: XU Jian G
TITLE OF INVENTION: A
TITLE OF INVENTION: C
TITLE OF INVENTION: S
TITLE OF INVENTION: E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY, AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REGISTRATION NUMBER: 17,98020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0:
FILING DATE: 14-JUN-1994
CLASSIFICATION: 435
                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 758 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-5600
TELEPAX: (415) 543-5043
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CORRESPONDENCE ADDRESS:
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                   STATE:
                                                                                                                                                                                      CITY: San Francisco
                                                                                                                                                                                                        ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 FNDIFHSGEGDDLL 14
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8; Conserv
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                                                                                                                              94111-3834
                                                                                                                                                                   California
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                                                                                                                                                                                                                                                                                                                                                                                            Hall, Robert H.
Xu, Jian Guo
                                                                                                                                               USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15) 543-9600
) 543-5043
) ID NO: 2:
                                                                                                                                                                                                                                                                    coli O157:H7 and its Use for the Rapid, Sensitive and Specific Detection of O157:H7 and Other Enterohemorrhagic E. coli
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57.1%;
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Pred. No. 0.75;
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APPLICATION NUMBER: FILING DATE: 11-SE

11-SEP-1995

US/08/526,813

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PCT-US95-08554-2
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GENERAL INFORMATION:
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Matches 8; Conserv
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                                                                                             TELEFAX: (415) 543-504
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 576-030 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 758 amino acids
                                                                                                             TELEFOMMUNICATION INFORMATION: TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC COMPUTER: PC DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION UNMERE: DATA:
ABBITCATION NUMBER: DCT/(1005/1005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: XU, Jian Guo
TITLE OF INVENTION: A NI
TITLE OF INVENTION: COLI
TITLE OF INVENTION: SPEC
TITLE OF INVENTION: E.
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MOLECULE TYPE: protein
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FILING DATE: 14-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: CARTCHI-UTOLOGY
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                     TOPOLOGY:
                                                                                                                                                                       NAME: Garrett-Wackowski, Eu REGISTRATION NUMBER: 37,330 REFERENCE/DOCKET NUMBER: 15
                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 14-JUN CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                   amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A NEW AND DISTINCTIVE DNA SEQUENCE OF E. COLI O157:H7 AND ITS USE FOR THE RAPID, SENSITIVE AND SPECIFIC DETECTION OF O157:H7 AND OTHER ENTEROHEMORRHAGIC E. COLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67.5%;
57.1%;
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                                                                                                                                                                                                                                                                                                                             Version
                                                                                                                                                                                                                                                                                                                                 #1.25
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RESULT 7
US-07-908-253-2
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US-08-619-812-8
                                                           Sequence 2, Application US/07908253 Patent No. 5534256
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Best Local :
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Best Local Similarity
Matches 8; Conserv
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                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (415) 327-32 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 15-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
FILING DATE: 29-MAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
APPLICANT: POTTER, ANDREW A.
APPLICANT: HARLAND, RICHARD J.
TITLE OF INVENTION: HAEMOPHILUS SOMNUS OUTER MEMBRANE
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 617-8999
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                                                                                                                                                   747 NDLLHGGKGDDI 758
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                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 33, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: ROBINS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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                                                                                                                                                                               2 NDIFHSGEGDDL 13
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                                                                                                                                                                                                             Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                              : 924 amino acids
amino acid
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HARLAND, RICHARD J.
RIOUX, CLEMENT R.
TVENTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UNITED STATES OF AMERICA
                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PatentIn Release #1.0,
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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58.3%;
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57.1%;
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Pred. No. 0.75;
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Pred. No. 2.
                                                                                                                                                                                                                Mismatches
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TITLE OF INVENTION:

PROTEIN EXTRACT ENRICHED WITH IRON-REGULATED PROTEINS

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Best Local Similarity
7; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: OJC
CITY: PALO ALTO
CTATE: CALIFORNIA
                                                                                                                                                                                                                                                                                             APPLICANT: REDMOND, MARK J.

APPLICANT: HUGHES, HUW P.A.

TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN

TITLE OF INVENTION: CHIMERAS

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 926 amino acids
TYPE: AMINO ACID
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FILING DATE: 19920702
CLASSIFICATION: 420
ATTORNEY/AGENT INFORMATION:
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                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM CC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                               STREET: 200 CITY: PALO ALTO
CITY: CALIFORNIA
CHATE: CALIFORNIA
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            APPLICATION NUMBER: 0
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REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEFAX:
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                                               CLASSIFICATION:
                                                           APPLICATION NUMBER: US/0
FILING DATE: 31-MAY-1995
                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 NDIFHSGEGDDL 13
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                                                                                                                                                                                                                                                                285 HAMILTON AVENUE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : (415) 617-8999
(415) 327-3231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                               UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                    POTTER, ANDREW A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ROBERTA L. ROBINS
                                                                                                                                                                                                                                                                                    REED & ROBINS
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14-OCT-1992
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                                                                             US/08/455,970A
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              US 07/960,932
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Pred. No.
                                                                                                                                                                                                                                                                  SUITE 200
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2.9;
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; TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-387-156-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Applic Patent No. 5723129
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07,
ETILING DATE: 16-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
                                                                                               TELEFAX: (415) 327-3231 INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 327-3400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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APPLICANT: REDMOND,
APPLICANT: HUGHES, H
                                                                                                                                  REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
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                                                                                SEQUENCE CHARACTERISTICS:
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| 747 NDLLHGGKGDDI 758
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                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                   NAME: ROBINS, ROBERTA L. REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 10-FE
                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn
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                                                                  LENGTH:
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                                                 amino acid
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                                                                  926 amino acids
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HUGHES, HUW P.A.
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                                 linear
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Pred. No. 2.9;
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; TOPOLOGY: linear ; MOLECULE TYPE: protein US-08-694-865-6
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Best Local Similarity
Thehes 7; Conserv
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US-08-878-748-6
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                                                                                                                                                     Sequence 6, Application US/08878748 Patent No. 5969126
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Best Local
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                                           GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: REDMOND, MARK J.
APPLICANT: HUGHES, HUW P.A.
TITLE OF INVENTION: GORH-LEUKOTOXIN CHIMERAS
NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/694,865
FILING DATE: 09-AUG-1996
CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS
STREET: 635 BRYANT STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: MCCRACKEN, THOMAS P.
REGISTRATION NUMBER: 38,548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: GRRH-LEUKOTOXIN CHIMERAS NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS: BOTTOS IIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: POTTER, ANDREW A. APPLICANT: MANNS, JOHN G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (415)327-3400
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                                                                                                                                                                                                                                                                                                                         Local Similarity les 7; Conserv
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CITY: PALO ALTO
STATE: CA
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                                                                                                                                                                                                                                                                                       2 NDIFHSGEGDDL 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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285 HAMILTON AVENUE, SUITE 200
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58.3%;
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58.3%;
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Pred. No. 2.
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Pred. No. 2.
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                                                                                                                                                                                                                                                                                                                                          DB 2;
2.9;
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2.9;
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RESULT 12
US-08-535-837-2
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Best Local
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,156
FILING DATE: 10-FEB-1995
APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/779,171
FILING DATE: 16-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: DOBTICE DOBTER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (415) 327-32 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 926 amino acids
TYPE: amino acid
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TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                        ADDRESSEE: ROBERTA L.
                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   747 NDLLHGGKGDDI 758
                                                                                                                                                                                                          STREET: 285 HAMILTON AVENUE, CITY: PALO ALFO STATE: CALIFORNIA COUNTRY. HAVENUE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: ROBINS, ROBERTA L. REGISTRATION NUMBER: 33,208
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                     APPLICATION NUMBER: FILING DATE: 27-SE
                                                                                                                                                                                                        COUNTRY:
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                                                                                                                                                                                                        UNITED STATES
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                                                 27-SEP-1995
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                                                                   US/08/535,837
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; TOPOLOGY: 1; MOLECULE TYPE: US-09-124-491-6
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Best Local S
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 amino acids
                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/694,865
APPLICATION NUMBER: US 08/387,156
APPLICATION NUMBER: US 08/387,156
FILING DATE: 10-FDB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/779,171
APPLICATION NUMBER: US 07/779,171
FILING DATE: 16-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                              TELEFAX: (415)327-3231 (NFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 327-3400 TELEFAX: (415) 327-3231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: POTTER, ANDREW A. APPLICANT: MANNS, JOHN G. TITLE OF INVENTION: GRRH-LEU
                                                                         SEQUENCE CHARACTERISTICS LENGTH: 926 amino acid
                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: MCCRACKEN, THOMAS P.
REGISTRATION NUMBER: 38,548
                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (415)327-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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2.9;
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RESULT 14
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Best Local Similarity
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; TITLE OF INVENTION: PASTEURELLA HAEMOLYTICA LEUKOTOXIN
; COMPOSITIONS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 07-APR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12, Application US/08455970A Patent No. 5708155
GENERAL INFORMATION:
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Best Local
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APPLICATION NUMBER: US/
FILING DATE: 09-FEB-1993
                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
DEFORM TO MINISTER BY 105 (155 070)
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: POTTER, ANDREW A
APPLICANT: REDMOND, MARK J.
APPLICANT: HUGHES, HUW P.A.
TITLE OF INVENTION: ENHANCE
TITLE OF INVENTION: CHIMERA
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             FILING DATE: 14-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,932
                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 504,850 FILING DATE: 05-APR-1990 APPLICATION NUMBER: 335,018
                                                                                         FILING DATE: 31-MAY-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                    CITY: PALO ALTO
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REGISTRATION NUMBER:
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58.3%;
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Pred. No. 2.
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REFERENCE/OCKET NUMBER: 9001-0016.10

TELEPHONE: (415) 227-3400;

TELEPHONE: (415) 227-340;

TELEPHONE: (415) 227-340;

TELEPHONE: (415) 227-340;

INTERPRES: (415) 227-340;

INTERPRES
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escherichia caenorhabdi chlamydia erwinia

Chr

drosophila

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Post-processing: Minimum Match
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LKTA_ACTAC
CYAA_BORPE
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 HLYA_SERMA
RBP1_PLAVB
HLYA_PROVIB
HLYA_PROVIB
HLYA_PROVIB
SLAP_BACST
SLAP_CAUCR
PMPD_CHLMU
RBP2_PLAVB
OMPB_RICRI
CAPA_PROMI
GTFE2_STROMO
PRTC_ERWCH
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RT32_ACTPL
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P16462
Q57506
Q57506
P55127
Q9jyv5
Q9jyv5
Q9byv9
P55126
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P55117
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5 neisseria m
9 neisseria m
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 SEQUENCE FROM N.A.

STRAIN-SEROTYPE A1 / PHL101;

MEDLINB-89210283; pubmed=2707:

Highlander S.K., Chidambaram I

"DNA sequence of the Pasteure.

Cluster":
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LKA1_PASHA

P16535;

01-AUG-1990

01-AUG-1990

30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-SEROTYPE A1;
MEDLINE-87306837; Publ
Lo R.Y.C., Strathdee (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 884-953 FROM N.A.

STRAIN-SEROTYPE A1 / PHLIO1;

MEDLINE=90236888; pubmed=2185213;

Highlander S.K., Engler M.J., Weinstock G.M.;

"Secretion and expression of the Pasteurella haemolytica Leukotoxin.";

"Secretion and expression of the Pasteurella haemolytica Leukotoxin.";

J. Bacteriol. 172:2343-2350(1990).

-i- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD

-i- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS NOT CLEARLY

CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                               "Nucleotide sequence of the leukotoxin (haemolytica Al.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence up
30-MAY-2000 (Rel. 39, Last annotation
Leukotoxin from serotype Al.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Infect.
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NCBI_TaxID=75985;
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                                                                                                                         ACTIVITY.

DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY) PTM: PALMITOYLATED BY LKTC. THE TOXIN ONLY BECOMES ACTIVE W
                                                                                                                                                                         SUBCELLULAR LOCATION: Secreted DOMAIN: THE GLY-RICH REGION IS CALCIUM, WHICH IS REQUIRED FOR
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                                                                                                               MODIFIED (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Immun.
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Chidambaram M., Engler M.J., Weinstock G.M.;
the Pasteurella haemolytica leukotoxin gene
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PM12_CCLLP
YFAL_ECOLI
YMJB_CAEEL
LMA3_HUMAN
YDBA_ECOLI
TOXB_CLODI
PRZN_SERMA
YDJA_ECOLI
OMPB_RICCN
SIAP_CAMFEE
LMA_DROME
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OR CYTOLYTIC
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6 escherichia
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4 serratia ma
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Match Query

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                                                                                                                                                                                                                                                                                                                                                                                                                                       Pasteurella haemolytica.
Bacteria; Proteobacteria;
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InterPro;
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DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO I
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PTM: PALMITOYLATED BY LKTC. THE TOXIN ONLY BECOMES ACTIVI
MODIFIED (BY SIMILARITY).

SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
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IPR003355; RTX_N.
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POTENTIAL.

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SEQUENCE FROM N.A.
MEDLINE-93239320; PubMed-8478098;
MEDLINE-93239320; PubMed-8478098;
Chang Y.-F., Ma D.-P., Shi J., Chengappa M.M.;
Chang Y.-F., Ma D.-P., Shi J., Chengappa M.M.;
"Molecular characterization of a leukotoxin gene"
"Molecular characterization of a leukotoxin gene"
"Molecular characterization of a leukotoxin gene"
                                                                                                                                                   PROSITE; PS00330; HEMOLYSIN_CALCIUM; 4. Hemolysis; Toxin; Cytolysis; Cytotoxin; Transmembrane; Lipoprotein; Palmitate.
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InterPro; IPR003355; RTX_N.
InterPro; IPR003995; RtxA.
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Bacteria; Proteobacteria; gamma
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DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE INVOLVED IN PORE FORMATION BY THE CYTOTOXIN PTM: PALMITOYLATED BY LKTC. THE TOXIN ONLY B MODIFIED (BY SIMILARITY).
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DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IS NOT HEMOLYTIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LANISTNLKNSLQSGLHKTGQSLNQAGQSLKAGAKKLILYIPKDYEYDSGRGNGLQDLVK
                                                                                      TALAAISGGVSAAAAGSLVGAPIALLVSGITGIISTILQYSKQAMFEHVANKIHDKIVDW
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DENKSQKLSASDIAS-SLNKLVGSMALFGTAN
                         FREADYAKTVHNYQAT-ADEKIEEIIGRQGERITSKQIDELIEKGKG--KIDQSELERIA
                                       Y----ITSNIQNYQSNKTDHKIEQLIGKDGSYITSDQIDKILQDKKDGTVITSQELKKLA
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                                                                            GNDILCTVKG-GNDSISDSGGNDRLSFADSNLKDLTFEKVNHHLMI-TNVKKEKVTIQNW
                                                                                                                            IFKGSKFDDAFHGGDGVDNIDGNAGNDRLFGGKGFDIIDGGDGDDFIDGGQGDDILHGGK
                                                                                                                                          VFKGSKFNDIFHSGEGDDLLDGGAGDDRLFGGKGNDRLSGDEGDDLLDGGSGDDVLNGGA
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                                                                                                                                                                                               RKVARGDIYHEVVKRQETKVGKRTETIQYRDYELRKVGYGYQSTDNLKSVEEVIGSQFND
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Pred. No. 1.8e-111;
3; Mismatches 252;
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Query Match Best Local Similarity

48. . 7%;

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01-OCT-1996
30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94041617; PubMed=8225575;
Burrows L.L., LO R.Y.C., Olah-Winfield
"Molecular analysis of the leukotoxin d
haemolytica serotypes 1 to 16.";
Infect. Immun. 61:5001-5007(1993).
Infect. Immun. 61:5001-5007(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-SEROTYPE T3;
REPEAT
REPEAT
SEQUENCE
                                                                                                                                                                                                                               InterPro;
InterPro;
                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Mannheimia.
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                                                                                                                                  !ransmembrane;
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DOMAIN: THE GLY-RICH REGION IS
CALCIUM, WHICH IS REQUIRED FOR
                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTIVITY
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IPR003355; RTX_N.
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(Rel. 34, Last sequence up
(Rel. 39, Last annotation
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297
381
734
                       ; Lipoprotein;
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97 318
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81 401
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s; Cytotoxin;
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6 X REPEATS,
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   FDBDCE2FDC85FDF2
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01-APR-1990
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            SEQUENCE FROM N.A.
STRAIN-SEROTYPE 5;
MEDLINE-90126233; PubMed-2693022;
Chang Y.-F., Young R., Struck D.K.;
"Cloning and characterization of a her (Haemophilus) pleuropneumoniae.";
DNA 8:635-647(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
DOMAIN
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InterPro; IPR003355; RTX_N.
InterPro; IPR003355; RTX_N.
Pfam; PF00353; hemolysinCabind; 1.
Pfam; PF00352; RTX; 1.
PRINTS; PR00313; CABNDNGRPT.
PRINTS; PR01488; RTXTOXINA.
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EMBL; X61111; CAA43423.1;
PIR; B33389; B33389.
PIR; S18853; S18853.
                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                              -
                                                                              REPEAT
                                                                                                                                                                   PROSITE; PS00330; HEMOLYSIN_CALCIUM; Hemolysis; Toxin; Cytolysis; Cytotox
                                                                                                                                                                                                                                                                                                                                                                                                                                         -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Cytolysins of Actinobacillus pleuropneumoniae
Infect. Immun. 59:4497-4504(1991).
-!- FUNCTION: ONE OF THE VIRULENCE FACTORS OF A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gielkens A.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Actinobacillus pleuropneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Cytolysin IIA) (CLY-IIA).
APXIIA OR CLYIIA OR HLYIIA OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000 (Rel. 39, Last annotation update) RTX-II toxin determinant A (APX-IIA) (Hemolys
                                                                                                                                                         Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Secreted.

DOMAIN: THE GLY-RICH REGION IS PROBABLY
CALCIUM, WHICH IS REQUIRED FOR TARGET CE
ACTIVITY (BY SIMILARITY).

DOMAIN: THE THREE TRANSMEMBRANE DOMAINS
INVOLVED IN PORE FORMATION BY THE CYTOTC
PTM: PALMITOYLATED BY APXIIC. THE TOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                   MODIFIED (BY SIMILARITY).
SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: ONE OF THE VIRULENCE FACTORS OF WHICH SHOWS A WEAK HEMOLYTIC ACTIVITY AND FOR ALVEOLAR MACROPHAGES AND NEUTROPHILS.
                                 233
266
361
361
719
719
728
728
737
746
764
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406
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            102531
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                   POTENTIAL.
POTENTIAL.
8 x REPEATS
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Cytotoxin;
                                                                                                                                              POTENTIAL.
           BDBCABBADF14A641 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Smith H.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hemolysin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Hemolysin
                                                                                                                                                                                                                                                                                                                                                                                                                                       OMAINS ARE BELIEVED TO BE CYTOTOXIN (BY SIMILARITY) TOXIN ONLY BECOMES ACTIVE
                                                                                                                                                                      Repeat;
                                                                                                                                                                                                                                                                                                                                      http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pleuropneumoniae)
Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                   Usage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A. PLEUROPNEUMONIAE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  serotype
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NNQISAEALSKVVNDYNTSK-DRONVSNSLAKLISSVGSFTSSSDFRNN
                       GTVITSQELKKLADENKSQKLSASDIASSLNKLVGSMALFGTANSVSSN
                                                                                                                                                                                      KSVEEVIGSQFNDVFKGSKFNDIFHSGEGDDLLDGGAGDDRLFGGKGNDRLSGDEGDDLL
                                                                                                                                                                                                                ATAETEKGSYSVKRYVGDSKALHETIATHQTNVGNREEKIEYR-REDDRFHTGYTVTDSL
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                                                                                                       VGGTGNDIISGGKDNDIYVHKTGDGNDSITDSGGQDKLAFSDVNLKDLTFKKVDSSLEI-
                                                                                                                                                             KSVEEIIGSQFNDIFKGSQFDDVFHGGNGVDTIDGNDGDDHLFGGAGDDVIDGGNGNNFL
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Pred. No. 7e-108;
88; Mismatches 254;
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STANDARD;

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NGIRSTLTATRGGLNRAGQSLTQAGQTLKNGAKKIILYIPKDYKYDSGSGNGLQDLVKAA Matches Query Match Best Local

Similarity

48.1%; 48.2%; 178;

Score 2236; DB 1; Pred. No. 1.2e-107; 8; Mismatches 271;

Length Indels

44;

17;

Conservative

---STKSGLKNLYLAIPKD--YDPQKGGTLNDFIKAA

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P55117;
01-OCT-1996
01-OCT-1996
30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pasteurella haemolytica serotype Al leukotoxin.";
Microbiology 142:2499-2507(1996).
-i- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK I DEFINED.
DEFINED.
-i- SUBCERIAL SAND CAUSE CELL RUPTURE BY MECHANICAL AND CAUSE CELL RUPTURE BY MECHANICAL AND CAUSE CELL RUPTURE BY MECHANICAL DEFINED.
REPEAT
SEQUENCE
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                                                                         REPEAT
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Pfam; PF00353; hemolysinCabind;
Pfam; PF02382; RTX; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 34, Created
01-OCT-1996 (Rel. 34, Last se
30-MAY-2000 (Rel. 39, Last an
Leukotoxin from serotype T10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR003355; RTX_N.
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                                                 REPEAT
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                                                                                                                                                                                                                                                               Transmembrane;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY) PTM: PALMITOYLATED BY LKTC. THE TOXIN ONLY BECOMES ACTIVE W MODIFIED (BY SIMILARITY).
SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
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DOMAIN: THE GLY-RICH REGION IS PROBABI
CALCIUM, WHICH IS REQUIRED FOR TARGET
                                                                                                                                                                                                                                                                                                                                 PR00313; CABNDNGRPT PR01488; RTXTOXINA.
                                                                                                                                                                                                                                                               Lipoprotein;
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Palmitate.
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on update)
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                                                                                                                                                                                                                                                                                     Repeat; Calcium;
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    CRC64;
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PRINTS; PR00313; CABNDNGRPT
PRINTS; PR01488; RTXTOXINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
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-!- DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY)

-!- PTM: PALMITOYLATED BY LKTC. THE TOXIN ONLY BECOMES ACTIVE W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=3714;
                                                                                                                                                                                                                                                                                                                                                               Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00353; hemolysinCabind;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M90440; AAA21918.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/
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SUBCELLULAR LOCATION: Secreted.
DOMAIN: THE GLY-RICH REGION IS
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                                                                                         KGGTLNDFIKAADELGIARLAEEPNHTETAKKSVDTVNQFLSLTQTGIAISATKLEKFLQ
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                                     KHSTNKLAKGLDSVENIDRKLGKASNVLSTLSSFLGTALAGIELDSLIKKGDAAPDALAK
                                                                                                                                          MSNINV--IKSNIQAGL---------NSTKSGLKNLYLAIPKDYDPQ
          ASIDLINEIIGNLSQSTQTIEAFSSQLAKLGSTISQAKGFSNIGNKLQNL-NFSKTNLGL
                                                                              QGNGIQDLVKAANDLGIEVWREERSNLDIAKTSFDTTQKILGFTDRGIVLFAPQLDNLLK
                                                                                                                      MSKITLSSLKSSLQQGLKNGKNKLNQAGTTLKNGLTQTGHSLQNGAKKLILYIPQGYDSG
{\tt AGLELTNELVGNIASSVQTVDAFAEQISKLGSHLQNVKGLGGLSNKLQNLPDLGKASLGL}
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   "Genetic map of the Actinobacillus pleuropneumoniae operons: characterization of the ApxIII operons."; Infect. Immun. 62:4411-4418(1994).
                                                                              STRAIN=405 / SEROTYPE 8;
MEDLINE=95012630; PubMed=7927703;
                                                                                             SEQUENCE FROM N.A. STRAIN=405 / SEROJ
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APXIIIA OR CLYIIIA OR RTXA OR PTXA
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EMBL; X68815; CAA48711.1;
InterPro; IPR001343; Hemly
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Pfam; PF02382; RTX; 1.
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Toxin; Cytolysis; Cytotoxin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ect. Immun. 61:947-954(1993).

FUNCTION: DOES NOT HAVE HEMOLYTIC ACTIVITY CATORICITY TOWARDS ALVEDLAR MACROPHAGES A SUBCELLULAR LOCATION: Secreted.

DOMAIN: THE GLY-RICH REGION IS PROBABLY INV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
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GSSTGDAVS-KLAKSQTIISGIQSVLGTVLAGINLNEAIISGGSELE-LAEAGVSLASEL
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426; Conser
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Mismatches 286:
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                                                                                           RT31_ACTPL STANDARD; PRT; 1049 AA. p55130; O1-OCT-1996 (Rel. 34, Created) O1-OCT-1996 (Rel. 34, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) 30-MAY-211I toxin determinant A from serotype 2 (AP) RTX-III toxin determinant A from serotype 2 (AP) APXIII OR CLY-IIIA). APXIIIA OR CLY-IIIA) (CLY-IIIA) (Rel. 39, Last annotation update) Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae (Haemophilu
Actinobacillus.
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Pfam; PF02382; RTX; 1.
PRINTS; PR00313; CABNDNGRPT.
PRINTS; PR01488; RTXTOXINA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genetic map of the Actinobacillus pleuropneumoniae operons: characterization of the ApxIII operons."; Infect. Immun. 62:4411-4418(1994).
-i- FUNCTION: DOES NOT HAVE HEMOLYTIC ACTIVITY BUT S
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Chang Y.-F., Shi J., Ma D.-P., Shin S.J.,
"Molecular analysis of the Actinobacillus
toxin-III gene cluster.";
DNA Cell Biol. 12:351-362(1993).
                                                                                                                                                                                                           Lipoprotein; TRANSMEM
                                                                                                                                                                                                                               PROSITE; PS00330; HEMOLYSIN_CALCIUM;
Toxin; Cytolysis; Cytotoxin; Repeat;
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EMBL; X80056; CAB37652.1; ALT_SEQ.
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR003355; RTX_N.
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Escherichia coli.";
J. Bacteriol. 178:5422-5430(1996).
-i- FUNCTION: BACTERIAL HEMOLYSINS
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PROSITE; PS00330; HEMOLYSIN_CALCIUM;
Hemolysis; Toxin; Cytolysis; Cytotox
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                                                                                                                                                                                                          Pfam; PF00353; hemolysinCabind; Pfam; PF02382; RTX; 1.
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Goebel W.;
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HLYA.
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"Nucleotide sequence of a plasmid-encoded hemolysin detern
its comparison with a corresponding chromosomal hemolysin
FBMS Microbiol. Lett. 34:1-11(1986).
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DISEASE: 7
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                                               use by non-profit institutions as modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
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FEBS Lett. 187:339-344(1985).
-I- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOCELL MEMBRANES AND CAUSE CELL RUPTURE I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-85234404; PubMed-3891743;
FelmLee T., Pellett S., Welch R.A.;
"Nucleotide sequence of an Escherichia
J. Bacteriol. 163:94-105(1985).
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DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE INVOLVED IN PORE FORMATION BY THE CYTOTOXIN.

PUM: PALMITOYLATED BY HLYC. THE TOXIN ONLY BECOMES ACTIVE
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DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
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TRANSMEM 267 326
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DOMAIN 723 869
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REPEAT 741 746
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InterPro; IPR003355;
InterPro; IPR003995;
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                                                                                                        VSGILSAISASFILSNADADTGTKAAAGVELTTKVLGNVGKGISQYIIAQRAAQGLSTSA
                                                                                                                                                                                          LAKGLDSVENIDRKLGKASNVLSTLSSFLGTALAGIELDSLIKK---
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MADVIAEWEKKH-GKNYFENGYDARHAAFLEDNFKILSQYNKEYSVERSVLITQQHWDTL
          EASLTTISTALGAVSAGVSAAAVGSAVGAPIALLVAGVTGLISGILEASKQAMFESVANR
                                                                     AAAGLIASVVTLAISPLSFLSIADKFKRANKIEEYSQRFKKLGYDGDSLLAAFHKETGAI
                                                                                     AVAALITSSIMLAISPLAFMNAADKFNHANALDEFAKQFRKFGYDGDHLLAEYQRGVGTI
                                                                                                                  ITGLLSGISAGFALADKNASTGKKVAAGFELSNQVIGNVTKAISSYVLAQRVAAGLSTTG
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PALMITATE (BY SIMILARITY).
A -> T (IN STRAIN 2001).
W; 196D5C0A9A2BB54D CRC64;
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STRAIN=13039 / SEROTYPE 10;
STRAIN=13039 / SEROTYPE 10;
MEDLINE=94,276850; PubMed=8007819;
Nagai S., Yagihashi T., Ishihama A.;
"DNA sequence analysis of an allelic va"
pleuropneumoniae RTX-toxin I (ApxIA) fi
Microb. Pathog. 15:485-495(1993).
                                                                                                                                                                                                                                                                                                                                (HLY-IA) (Cytolysin IA) (CLY-IA)
APXIA OR CLYIA OR HLYIA.
Actinobacillus pleuropneumoniae
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30-MAY-2000
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01-OCT-1996
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                           Chin N., Frey J., Chang C.F., Chang "Identification of a locus involved Actinobacillus pleuropneumoniae."; FEMS Microbiol. Lett. 143:1-6(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        RT12_ACTPL
                                                                                           STRAIN=K17 / SEROTYPE 5;
MEDLINE=96401417; PubMed=8807793;
                                                                                                         SEQUENCE FROM N.A. STRAIN-K17 / SEROT
                                                                                                                                                                                                                                                                                 Actinobacillus.
NCBI_TaxID=715;
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T-1996 (Rel. 34, Last sequence update)
Y-2000 (Rel. 39, Last annotation update)
toxin determinant A from serotypes 5/10
Ta) (Cytolysin IA) (CLY-IA).
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   886-1023
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Pasteurellaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003995; RtxA.
Pfam; PF00353; hemolysinCabind;
Pfam; PF02382; RTX; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jansen R., Briaire J., Kamp E.M., Gielkens 
"Structural analysis of the Actinobacillus 
I (ApxI) operon ":
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                                                                                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                                       Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                 Hemolysis; Toxin; Cytolysis;
                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00330; HEMOLYSIN_CALCIUM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
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                                              Local
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SUBCELLULAR LOCATION: Secreted.
DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOL. ACTIVITY.
DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY) DOMAIN: PALMITOXLATED BY APXIC. THE TOXIN ONLY BECOMES ACTIVE FORMATION BY THE TOXIN ONLY BECOMES ACTIVE FORMATION BY APXIC. THE TOXIN ONLY BECOMES ACTIVE FORMATION BY APXIC.
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MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF SEROTYPE
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                                   404;
                                              Similarity
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.6e-82;
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YGEGYNALPQLRKDIEQIISSTGALTGEHGQVLVGAGGPLAYSNSPNSIPNAFSNYLTQ
                           ADENKSQ----KLSASDIASSLNKLVGS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Actinobacillus pleuropneumoniae
Bacteria; Proteobacteria; gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2000 (Rel. 39, Last annota RTX-I toxin determinant A from se (HLY-IA) (CQYtolysin IA) (CLY-IA) APXIA OR CLYIA OR HLYIA.
                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Chang Y., Wang Y., Chin N.;
Submitted (JAN-1994) to the EMBL/GenBank/DDBJ
SUBMITTED CONTROL OF THE VIRTLENCE FACTORS OF
-IP FUNCTION: ONE OF THE VIRTLENCE FACTORS OF
WHICH HAS A STRONG HEMOLYTIC ACTIVITY AND
ALYEOLAR MACROPHAGES AND NEUTROPHILS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-ISOLATE CVI 13261 / SEROTYPE 9;
MEDLINB-9336425; PubMed-8359891;
Jansen R., Briaire J., Kamp E.M., Gielkens
"Structural analysis of the Actinobacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Frey J., Haldimann A., Nicolet J., Boffini A., "Sequence analysis and transcription of the apx from Actinobacillus pleuropneumoniae."; Gene 142:97-102(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM
STRAIN=S 4074
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STRAIN=S 4074 / SEROTYPE
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STRAIN=S 4074 / SE
PRINTS; I
PRINTS; I
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                                                              InterPro; IPR001343; Hemlysn_Ca_bind
InterPro; IPR003355; RTX_N.
InterPro; IPR003995; RtxA.
                                                                                                                                                                                                                                                                                 8, 12, AND TOTALLY DELETED IN SEROTYPE 3.
MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF SEROTYPE 1
SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY
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DOMAIN: THE GLY-RICH REGION IS
CALCIUM, WHICH IS REQUIRED FOR
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MISCELLANEOUS: APXIA IS F
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DOMAIN: THE THREE
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                                       PF00353; hemolysinCabind; PF02382; RTX; 1.
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              PR00313;
PR01488;
  PS00330; HEMOLYSIN_CALCIUM;
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pasteurellaceae;
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A. PLEUROPNEUMONIAE
IS CYTOTOXIC FOR
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HIGEKNDRIYLSSGSSIYYAGNGHDVAYYDKTDTGY--LTEDGQSAQKAGEYIVTKELKA
              \texttt{KAG--NDDIFVGQGKMNIDGGDGHDRVFYSK-DGGFGNITVDGTSATEAGSYTVNRKV+A}
                                          SRERLINGKYSYINKLKFGRVKNWQVTDGEASSKL-DFSKVIQRVAETEGTDEIGLIVNA
                                                                   KSGKAYVDFFEEGKLLEKEPDRFDKKVFDPLEGKIDLSSIN--KTTLLKFVTPVFTAGEE
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TC -> R (IN REF. 3 AND 4).
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Lally E.T., Golub E.E., Kleba I.R., Taichm
Rosenbloom J.C., Gibson C.W., Demuth D.R.;
"Analysts of the Actinobacillus actinomyce
gene. Delineation of unique features and c
                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                              entities requires or send an email t
                                                                               use by non-profit institutions as long modified and this statement is not removed.
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NCBI_TaxID=714;
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Bacteria; Proteobacteria;
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DOMAIN: THE THREE TRANSMEMBRANE DOMAINS ARE BELIEVED TO BE INVOLVED IN PORE FORMATION BY THE CYTOTOXIN (BY SIMILARITY). PTM: PALMITOYLATED BY LKTC. THE TOXIN ONLY BECOMES ACTIVE WH MODIFIED (BY SIMILARITY).

DISEASE: ITS TARGET CELL SPECIFICITY IS RESTRICTED TO HUMAN SOME NON-HUMAN CELLS OF THE MONOMYELOCYTIC LINEAGE.
SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
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DOMAIN: THE GLY-RICH REGION IS
CALCIUM, WHICH IS REQUIRED FOR
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                              a license agreement (See http://www.isb-sib.ch/announce/
to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00353; hemolysinCabind; Pfam; PF02382; RTX; I. RFNTS; PR00313; CABNDGRPT. PRINTS; PR01488; RTXTOXINA.
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InterPro; IPR003355;
InterPro; IPR003995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
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HSSP; P04002; 1WFA.
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                                                                         DKNASTGKKVAAGFELSNQVIGNVTKAISSYVLAQRVAAGLSTTGAVAALITSSIMLAIS
                                                                                                                                                                                                      EAFSSQLAKLGSTISQAKGFSNIGNKLQNL----NFSKTNLGLEIITGLLSGISAGFALA
                                                                                                                                                                                                                                 QSVLGTLQAFLNTAFSGMDLDALIKARQNGKNVTDVQLAKASLNLINELIGTISSITNNV
                                                                                                                                                                                                                                            SNVLSTLSSFLGTALAGIELDSLIK---KGDAAPDA-LAKASIDLINEIIGNLSQSTQTI
                                                                                                                                                                                                                                                                                                             NIDAAKEQLQKALDKLGKTGKKLTLYIPKNY--KKGNGLTALIKAAQKLGIEVYHEGKDG
          SGKAYADAFEDGKKVEAGSN----ITLDAKTGIIDISNSNGKKTQALHFTSPLLTAGTES
                                               NYFDKGYDSRYAAYLANNLKFLSELNKELEAERVIAITQQRWDNNIGELAGITKLGERIK
                                                                                                                          PLAFMNAADKFNHANALDEFAKQFRKFGYDGDHLLAEYQRGVGTIEASLTTISTALGAVS
                                                                                                                                                                                             DTFSKQLNKLGEALGQVKHFGSFGDKLKNLPKLGNLGK---GYGALSGVLSAISAALLLA
                                                                                                                                                                                                                                                                      PALTNGILNTGKKLLGLTERGLTLFAPELDKWIQGNKHLSNSVG----STGNLTKAIDKV
                                                                                                                                                                                                                                                                                TETAKKSVDTVNQFLSLTQTGIAISATKLEKFLQ--KHSTNKLAKGLDSVENIDRKLGKA
SGKAYVDYLKKGEELAKHSDKFTKQILDPIKGNIDLSGIKGSTT--LTFLNPLLTAGKEE
                                     NYSENGYDARHSAFLEDSLKLFNELREKYKTENILSITQQGWDQRIGELAGITRNGDRIQ
                                                                                                                PLSFLGIAKQFDRARMLEAYSKRFKKFGYNGDSLLGQFYKNTGIADAAITTINTVLSAIA
                                                                                                                                                      NKHADTATKAAAAAELTNKVLGNIGKAITQYLIAQRAAAGLSTTGPVAGLIASVVSLAIS
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392; Conserv
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milarity 41.3%;
Conservative 16
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                                                                                                                                                                                                                                                                                                                                                                                                   114194 MW;
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Palmitate.
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87.55.43.11
                                                                                                                                                                                                                                                                                                                                                Score 1716.5; DB Pred. No. 6.6e-81; 7; Mismatches 291
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CYAA_BE

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P15318;

01-APR-1990 (Rel. 14, Created)

01-APR-1990 (Rel. 14, Last sequence update)

01-MAR-2002 (Rel. 41, Last annotation update)

01-MAR-2002 (Rel. 41, Last annotation update)

Bifunctional hemolysin-adenylate cyclase precursor (Cyclolysin) (ACT)

(AC-HLY) [Contains: Calmodulin-sensitive adenylate cyclase (EC 4.6.1.1) (ATP pyrophosphate-lyase) (Adenylyl cyclase); Hemolysin]
                                                                                                                          domains
Eur. J.
                                                                                                                                                                                                                                                                                          MEDLINE-89091151; PubMed-2905265; Glaser P., Sakamoto H., Bellalou J., Ullmann A., Da "Secretion of cyclolysin, the calmodulin-sensitive haemolysin bifunctional protein of Bordetella pertu EMBO J. 7:3997-4004(1988).
     Danchin
                           Glaser P., Elmaoglou-Lazaridou
                                                  MEDLINE=89251630;
                                                                         MUTAGENESIS
                                                                                                                                                                       "Isolation
                                                                                                                                                                                              Munier H.,
                                                                                                                                                                                                                        MEDLINE=91177021;
                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=18323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glaser P., Ladant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-88216178;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      er P., Ladant D., Sezer O., Pichot F., Ullmann calmodulin-sensitive adenylate cyclase of Boroing and expression in Escherichia coli.";
Microbiol. 2:19-30(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YHEVVKRQETKVGKRTETIQYRDYEL--RKVGYGYQSTDNLKSVEEVIGSQFNDVFKGSK
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                                                                                                                          of Bordet
Biochem.
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                                                                                                                       and characterization of catalyt
Bordetella pertussis adenylate
ochem. 196:469-474(1991).
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                                                                                                                                                                                            PubMed=2007407;
A.-M., Glaser P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=2897067;
                                                     PubMed=2542030;
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                                                                                                                                              cyclase.
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                              Ladant
                                                                                                                                                                     A., Sarfati R., Barzu O. and calmodulin-binding
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Bordetella pert
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adenylate
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InterPro; IPR001343; Hemlysn\_Ca\_b
InterPro; IPR003355; RTX\_N.
InterPro; IPR003355; RTXA.
InterPro; IPR00395; RtxA.
Pfam; PF00353; hemolysinCabind; 5
Pfam; PF02382; RTX; 1.
PRINTS; PR00313; CABNDNGRPT.

5

PROSITE; PRINTS;

PS00330;

PR01488;

RTXTOXINA

HEMOLYSIN\_CALCIUM;

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PIR;

S00893; OYBRC. S09403; S09403.

Hemlysn\_Ca\_bind

EMBL; EMBL; EMBL;

EMBL;

Y00545; CAA68613.1; -. X14199; CAA32411.1; -. A07292; CAA00653.1; -. A14850; CAA01202.1; -.

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http://www.isb-sib.

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modified and this statement is entities requires a license or send an email +
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BASSIT T., Havilcek V., Bezouskova S., Halada P., Hackett M., Sebo P.;

"The conserved lysine 860 in the additional fatty-acylation site of Bordetella pertussis adenylate cyclase is crucial for toxin function independently of its acylation status.";

J. Biol. Chem. 274:10777-10783(1999).

J. BIOL. CHEM. 274:10777-10783(1999).
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Hackett M., Guo L., Shabanowitz J
"Internal lysine palmitoylation in
Bordetella pertussis.";
Science 266:433-435(1994).
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"Phylogeny of
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PALMITOYLATED BY CYAC. THE
MODIFIED IN POSITION LYS-983.
- SIMILARITY: IN THE N-TERMINAL SI
CLASS-2 FAMILY.
- SIMILARITY: IN THE C-TERMINAL SI
PROKARYOTIC TOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                              CELLS BY ELEVATING CAMP-CONCENTRATION AND THUS DI
CELL FUNCTION.
CATALYTIC ACTIVITY: ATP = 3',5'-cyclic AMP + diph
ENZYME REGULATION: ACTIVATED BY HOST CALMODULIN.
SUBCELLULAR LOCATION: Secreted.
DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED
CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDIN
ACTIVITY (BY SIMILARITY).
                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation
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DKLAQESSAYGYEGDALLAQLYRDKTAAEGAVAGVSAVLSTVGAAVSIAAAASVVGAPVA
                                     DEFAKQFRKFGYDGDHLLAEYQRGVGTIEASLTTISTALGAVSAGVSAAAVGSAVGAPIA 369
                                                                                                               GNVTKAISSYVL----AQRVAAGLSTTGAVAALITSSIMLAISPLAFMNAADKFNHANAL
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H->R, P, L. LOSS OF ACTIVITY.

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H->R, P, L. LOSS OF ACTIVITY.

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E-SO, K: LOSS OF ACTIVITY.

317506 MW; F00744524BD442E CRC64;
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HEMOLYSIN HLYA).
A, CATALYTIC.
B, ALA/GLY-RICH.
C.
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ATP (POTENTIAL).
28 X REPEATS, GLY-RICH.
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	MGQGGDDTV 1287	1279	DЪ
	LQDKKDGTV 864	856	Qy
1278	RIVAPHEYGFGIEADLSREWVRKASALGVDYYDNVRNVENVIGTSMKD-VLIGDAQANTL 1278	1220	DЬ
855	SINIPRWYITSNLONYQSNKTDHKIEQLIGKDGSYITSDQIDKI	812	Qy
1219	RGGDDILRGGLGLDTLYGEDGNDIFLQDDETVSDDIDGGAGLDTVDYSAMIHPG	1166	DВ
811	GAGNDVYIFRKGDGNDTLYDGTGNDKLAFADANISDIMIERTKEGIIVKRNDHSG	757	Qy
1165	GIHADLQKGTVEKWPALNLFSVDHVKNIENLHGSRLNDRIAGDDQDNELWGHDGNDTIRG	1106	Db
756	NDRLSGDEGDDLLDGGSGDDVLNG 756	733	Qy
1105	NDTLVGGEGQNTVIGGAGDDVFLQDLGVWSNQLDGGAGVDTVKYNVHQPSEERLERWGDT 1105	1046	DЪ
732	DDRLFGGKG	724	Qy
1045	NVQYRHVELARVGQVVE-VDTLEHVQHIIGGAGNDSTTGNAHDNFLAGGSGDDRLDGGAG	987	Db
723	TIQYRDYELRKVGYGYQSTDNLKSVEEVIGSQFNDVFKGSKFNDIFHSGEGDDLLDGGAG	664	Qy
986	GGAGTNTVSYAALGRQDSITVSADGERFNVRKQLNNANVYREGVATQTTAYGKRTE	931	Db
663	GGDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNRKVARGDIYHEVVKRQETKVGKRTE	604	Qy
930	GKQDRWRIRDGAADTTIDLAKVVSQLVDANGVLKHSIKLDVIGGDGDDVVLANASRIHYD	871	Db
603	GRVKNWQVTDGEASSKLDFSKVIQRVAETEGTDEIGLIVNAKAGNDDIFVGQGKMNID	546	Qy
870	V-AGQPVVLDVAAGGIDIASRKGER-PALTFITPLAAPGEEQRRRTKTGKSEFTTFVEIV	813	망
545	VEAGSNITLDAKTGIIDISNSNGKKTQALHETSPLLTAGTESRERLTNGKYSYINKLKF- 545	487	Qy
812	SDGLRKMLADLQAGWNASSVIGVQTTEISKSALELAAITGNADNLKSVDVFVDRFVQGER 812	753	Db
486	NLKFLSELNKELEAERVIAITQQRWDNNIGELAGITKLGERIKSGKAYADAFEDGKK	430	Qy
752	VVTSLLTGALNGILRGVQQPIIEKLANDYARKI:DELGGPQAYFEKNLQARH-EQLAN 752	697	Дb
429	LLVAGVTGLISGILEASKQAMFESVANRLQGKILEWEKQNGGQNYFDKGYDSRYAAYLAN	370	Qy

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## ALIGNMENTS

REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS TITLE VERSION
KEYWORDS
SOURCE
ORGANISM RESULT AF205359 LOCUS DEFINITION ACCESSION JOURNAL 11497442 2 (bases l (bases 1 to 2784)
Angelos,J.A., Hess,J.F. and George,L.W.
Cloning and characterization of a Moraxella bovis cytotoxin gene
Am. J. Vet. Res. 62 (8), 1222-1228 (2001)
21388402 2 (bases 1 to 2784)
Angelos,J.A., Hess,J.F. and George,L.W.
Direct Submission
Submitted (15 NOV-1999) Veterinary Medicine/Epidemiology,
University of California, Davis, 2108 Tupper Hall, Davis, Moraxella bovis RTX toxin (mbx $\hat{\mathbf{A}}$ ) gene, complete cds. AF205359 AF205359.1 GI:15146407 Moraxella bovis Moraxella bovis Bacteria; Proteobacteria; AF205359 2784 gamma subdivision; Moraxellaceae; ģ DNA linear BCT 02-OCT-2001 S

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Unclassified.

1 (bases 1 to 3311)

1 (bases 1 to 3311)

RS Potter, A., Campos, M. and Hughes, H.P.A.

Vaccines with chimeric protein comprising gar
leukotoxin derived from pasteurella haemolyt
(NAL Patent: US 6096320-A 1 01-AUG-2000;
Location/Qualifiers

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Sequence 1 :
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AR104900.1
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       -tatgatccgcaaaaaggtgggactttaaaatgattttattaaaagctgctgatgaatt
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                                                             Score 815.6; DB 6;
Pred. No. 3.8e-133;
0; Mismatches 964;
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US 6096320
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109 taaattcaacgacatattccatagtggtgaaggtgatgatttactcgatggtggtggtgctgg 216	Qy 2 Db 2
049 taatttgaaatcagtagaagaagtaattggttctcaatttaatgatgtattcaaaggttc 21 	Qy 2 Db 2
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929 aggtgatatctaccatgaagttgtgaagcgtcaagaaaccaaggtgggtaaacgtactga 198 	2 1
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710 tgtagccgagacagaaggcacagacgagattggtctaatagtaaatgcaaaa	Qy 1. Db 2
650 ctggcaagttacagatggagaggctagttctaaattagatttctctaaagttattcagcg 170	Qу 1 Db 2
590 acgtttaactaatggtaaatactcttatattaataagttaaaattcggacgtgtaaaaaa 164 	Qy 1:
530 aaaaacycaagcyttycatttcacttcycctttyttaacaycagyaactyaatcacytya 158 	Qy 1: Db 2:
470 ttccaatattactttggatgctaaaactggtatcatagacattagtaattcaaatgggaa 152 	Qy 1,
1410 cattaagagcggaaaagcttatgcagatgcttttgaagatggcaagaaagttgaagctgg 1469 	Qy 1,
350 ccaacaacgttgggataataatattggtgagttagcaggtattaccaaattgggtga 	Qy 13 Db 18
1290   Cttaaaatttttgtctgagctaaataaagagttggaagctgaacgtgttattgcaatcac   1349	Qy 12 Db 17
230 cggtcagaactattttgataaaggctatgattctcgttatgctgcttatttagctaataa 1289	Qy 12 Db 17

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REFERENCE
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AGGCTCAGTATTGGCTGGAATGGATTTAGATGAGGCCTTACAGAA---TAACAGCAACCA
             gggcactgcattagcgggtatagaacttgattctttaatcaaaaaaggtgatgctgcacc
                                           TGATAAATTGCTACAGAAA-----ACTAAAGCAGGCCAAGCATTAGGTTCTGCCGA
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133956
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Potter,A., Campos,M. and Hughes,H.P.A.
Chimeric protein comprising an RTX-family
Interferon-2 or interferon
Patent: US 5594107-A 1 14-JAN-1997;
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Pred. No. 3.8e-133;
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                                                                    cattaagagcggaaaagcttatgcagatgcttttgaagatggcaagaaagttgaagctgg
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4 (bases 2 to 6 the Leukotoxin Mosaic Structure and Molecular Evolution of the Leukotoxin (Notable) in Mannheimia (Pasteurella) haemolytica, Mannheim glucosida, and Pasteurella trehalosi
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LLFSTIFFAVEMYYSPSHLTLVILGSLDCYILMSIFISPILRRRLDEKFRRSDNOAFI-
VESVTSINMIKAMAVAPOMTDTWDKOLASYVSSSFRVTVLATIGQOGVOLIQKTVMVI
NUMLGAHLVISGDLSIGQLIAFNMLSGGVIAFVIRLAOLWODFOQVGISVTRLGDVLN
SPTEDYQGKLSLPEIKGDISFKNIFFBYKFDAFTILMVNLDEIRQGFVGITVGRSGSG
KSTLTKLLQRFYIPENGOVLIDGHDLALADPNWLRGOIGVVLQDNVLLNRSIRENIAL
SDPGMPMERVIXAAKLAGAHDFISELREGYNTIVGEGGAGLSGGQORATAIARALVNN
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/db_xref="G1:150495"
/db_xref="G1:150495"
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EQDAPQILSQDEFEACYQGQLILVTSRASVVGQLAKFDFTWFIPAVIKYRKIFLETLI
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Mosaic Structure and Molecular Evolution of the Let (lktCABD) in Mannheimia (Pasteurella) haemolytica, glucosida, and Pasteurella trehalosi
J. Bacteriol. 184 (1), 266-277 (2002)
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Direct Submission
Submitted (04-OCT-2001) Institute of Biomedical
Division of Infection and Immunity, University of
Black Building, University Avenue, Glasgow G12 &
Sequence update by submitter
On Oct 9, 2001 this sequence version replaced gi
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                                                                                                                                   CTAAAAAATCATTCTCTATATACCAAAAGATTACAAATATGATTCAGGTAGTGGTAATG
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/db_xref="GI:15987956"
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FAYVRKYEGATRIEGEKLKDFKALYKOKSLSKHELLAGENKLIEAQNELAVYRSKLNE
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PYRRYGYLTGRIKHISPDAIEQFMVGLVENATISIDKKNLSSPDGRTIELGSGMTITA
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SPTEQYGAKLAGALAGTISELREGYNTIVGEGGAGLSGGORGRIAGALVNN
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MKFLLNLNKELQAERVIAITQQQWDSNIGDLAGISRLGEKVLSGKAYVDAFEEGQHLK
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Davies,R.L., Whittam,T.S. and Selander,K.A.
Direct Submission
Submitted (04-OCT-2001) Institute of Biomedical
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Direct Submission
Submitted (18-OCT-2000) Institute of Biomedical and Life Sciences
Division of Infection and Immunity, University of Glasgow, Joseph
Black Building, University Avenue, Glasgow G12 8QQ, Scotland
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J. Bacteriol. 184 (1),
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tagcagaagagcotaatcacactgaaacagcaaaaaaaatctgttgacacagtaaatcagt
                                CAAAAACTGGGGCAAAAAAATTATCCTCTATATTCCCCCAAAATTACCAATATGATACTG
                                                                                          CGACAAGAGACGATAAAATTGAAGAGATTATCGGTCAAAATGGTGAACGGATTACCTCGA
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Sequence
AR054439
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Potter, A.A. and Manns, J.G.
GnRH-leukotoxin chimeras
Patent: US 5837268 A 5 17 NOV-1998;
                                                                                                                                                                                                                                                                            Unclassified
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487 c 599 g
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patent US 5837268
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                                                                                                                        Score 814.4; DB 6;
Pred. No. 6.2e-133;
0; Mismatches 956;
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1303 1276	ttgataaaggctatgattctcgttatgctgcttatttagctaataacttaaaatttttgt	1244 1217
1243 1216	.ttacaaggtaaaattttagagtgggaaaagcaaaatggcg 	1184 1157
1183 1156	ttacaggattgatctctggaattttagaagcgtctaaacaggcaatgtttgaaagtgtttg 	1124 1097
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1003 976	ttccgaaaatttggctatgatggggatcatttattggctgaatat 	944 917
943 916	CATTTGCCGGTATTGCCGATAAATTTAATCATGCAAAAAGTTTAGAGAGTTATGCCGAAC	884 857
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823 796	atgtaacaaaagcaatttottcatatgttttagcacaacgtgttgctgctggtctatcaa 	764 737
763 736	atgcatcgactggcaaaaaagttgctgcaggttttgaattaagcaatcaagttattggta	704 677
703 676	tggaaataattactggtttgctatcaggcatttctgcaggctttgctttagcggataaaa	644 617
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526 496	aagctagtattgacttgattaatgagataattggtaatctatct	467 437
466 436	cgggtatagaacttgattctttaatcaaaaaaggtgatgctgcacctgatgctttggcta	407 380
406 379.	aattaggtaaagcaagtaatgtattatcaacattaagctctttttttgggcactgcattag	347 320
346 319	tcta	287 269
286 268	CtCacacaaactggtattgctatttctgcaacaaaattagaa 	227 209
208	AAAGAGAAGAACGCAATAATATTGCAACAGCTCAAACCAGTTTAGGCACGATTCAAACCG	149

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2362	gtgatggtaatgatactttgtacgatggcacgggcaatgataattagcatttgcagatg 	2303	Dh Qy
9	TAAAGGCAACGACCTATTACACGGTGGCAAGGGCGATGATATTTTCGTTCACCGTAAAG	23	Db
2302	gatgatgtattaaatggtggtgctggtaatgatgtctatatctttcggaaag	2243	Qy
2230	AAAGGCGATGATATTCTCGATGGTGAAAATGGTGATGATTTTATCGATGGCG	2171	Db
	tggtggtaaaggcaacgatcgactttctggagatgaaggcgatgatttactcgatggcg	18	Qy
2170	CCTTTAACGGTGGTGATGGTCGATACTATTGACGGTAACGACGCCAATGACCGCTTAT	2111	Db
2182	rtccatagtggtgaaggtgatgatttactcgatggtggtgctggtgacgaccgcttgt	2123	Qy
2110	TTGAAGAATTATCGGTACATCACATAACGATATCTTTAAAGGTAGTAAGTTCAATGATG	2051	DЪ
2122	agaagaagtaattggttotoaatttaatgatgtattoaaaggttotaaattoaacgaca.	90	Qy
2050	AACCAGCACCATGCCGGTTATTACACCAAAGATACCTTGAAAGCTG	1994	Db
2062	tgattatgaattaagaaaagttgggtatggttatcagtctaccgataatttgaaatcag	2003	Qy
1993	CTTCAACCCATACCGCATTAGTGGGCAACCGTGAAGAAAAATAGAATATC	1934	Db
2002	yaagttgtgaagcgtcaagaaaccaaggtgggtaaacgtactgaaactatccagtatc	9	γQ
1933		1874	Db
1942	caacagaagcaggcagttatacagttaatcgtaaggttgctcgaggtgatatctacc	8	Qy
1873	ACGACCGAGTTCACTATAGCCGTGGAAACTATGGTGCTTTAACTATTGATGCAACCA	1817	Db
1882	gatogtgtottotatagtaaagaoggaggatttggtaatattactgtagatggtaoga	.82	Qy
1816	TTTGTTGGTTCTGGTACGACGGAAATTGATGGCGGTGAAGGTT	1757	Db
1822	ggcaatgacgatatctttgttggtcaaggtaaaatgaatattgatggtggagatggac	7	Qy
1756	AACTAAAACCAAAGAAACAAAAATTATTGCCAAACTTGGTG	1697	Db
1762	aggcacagacgagattggtctaatagtaaatgcaaaag	1724	Qγ
1696	ATGGTGCAGCAAGTTCTACCTTTGATTTAACTAACGTTGTTCAGCGTATTGGTATTGAAT	1637	Db
1723	tggagaggctagttctaaattagatttctctaaagttattcagcgtgtagccgagacag	Ġ	Оу
1636	GAATATATTACCAAGCTCAATATTAACCGTGTAGATAGCTGGAAAATTACAG	1577	Db
1663	taaatactcttatattaataagttaaaattcggacgtgtaaaaaactggcaagttacag	6	Qy
1576	TCTTATTCAGAACGCCATTATTGACGCCGGGAACAGAGCATCGTGAACGCGTACAAACAG	1517	Db
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1516	AGCATA	1457	Db
1543	ggatgctaaaactggtatcatagacattagtaattcaaatgggaaaaaaacgcaagcgt	4	Qy
1456	 GATAAATTAGTACAG	w	Db
1483	cttatgcagatgcttttgaagatggcaagaaagttgaagctggttccaatattactt	1424	Qy
1396	ATAACAACATTGGTGATTTAGCTGGTATTAGCCGTTTAGGTGAAAAAGTCCTTAGTGGTA	w	Db
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1336	TTAAACAAAGAGTTACAGGCAGAACGTGTCATCGCTATTACTCAGCAGCAATGGG	1277	Db
1363	gctaaataaagagttggaagctgaacgtgttattgcaatcacccaacaacgttgg	1304	Qy

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REFERENCE
AUTHORS
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KEYWORDS
SOURCE
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                AAGCTGGCTTGGAGCTAACAAATTCATTAATTGAAAATATTGCTAATTCAGTAAAAAACAC
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                                                                                                           ATGCAAATAAAGCCAAAACTGTATTATCTGGCATTCAATCTATTTTAGGCTCAGTATTGG
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Sequence
AR081029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 2794)
Potter,A.A. and Manns,J.G.
GNRH-leukotoxin chimeras
Patent: US 5999126-A 5 19-OCT-1999;
Location/Qualifiers
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TCTTATTCAGAACGCCATTATTGACGCCGGGAACAGAGCATCGTGAACGCGTACAAACAG
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Potter, A. A. and Harland, R.J.
Haemophilus somnus outer membrane pro
iron-regulated proteins
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AGCGGATCACCTCAAAGCAAGTTGATGATCTTAT
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VERSION KEYWORDS SOURCE REFERENCE AUTHORS TITLE RESULT 1 BD009870 LOCUS COMMENT ACCESSION DEFINITION JOURNAL ORGANISM 1 (bases 1 to 2794)

Potter, A.A. and Manns, J.G.
GnRH-leukotoxin chimeras
Patent: JP 2001502887-A 3 06
UNIVERSITY OF SASKATCHEWAN
OS Unidentified
PN JP 2001502887-A/3
PD 06-MAR-2001
PF 08-AUG-1997 JP 19985091
PF 08-AUG-1996 US 08/69
PI ANDREW A POTTER, JOHN G
PC C12N15/16, C12N15/31, C12 BD009870.1 JP 200150288 GnRH-leukotoxin chimeras BD009870 unidentified BD009870 unclassified unidentified A61K38/09, C A61K39/385 2001502887-A/3 Unidentified

1P 2001502887-A/3

1P 2001502887-A/3

06-MAR-2001

08-AUG-1997 JF 1998509192

09-AUG-1996 US 08/694865

09-AUG-1996 US 08/694865

ANDREW A POTTER, JOHN G MANNS

ANDREW A POTTER JOHN G MANNS

C12N15/16,C12N15/31,C12N15/62,C12N1/21,C07K14/285, 2794 06-MAR-2001; đq DNA linear  $_{PAT}$ C07K7/23, 31-JAN-2002

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                       CAACTGGGCCTGTGGCTTTAATTGCTTCTACTGTTTCTCTTGCGATTAGCCCCATTAG
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487 c 599 g 77
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### PARTIFICCCGTATTGCCGTATTGATCHANAAGTTTAGAGAGTTTAGAGAGTTTAGAGAGTTTAGCGAAAAAGTTTAGCCGAAAAATTAATT	Qy	Db 5	٥٧	Db	ΟV	Оу Db	Db	Qy	Db	Qy	DЪ	Qy	Db	Qy	Db	Qy	Db	Oy	Db	Qy	Db	Qy	Db	Qy	Дb	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db
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        aaaaaggtgggactttaaatgattttattaaagctgctgatgaattaggtattgctcgtt 166
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                                      CAAAAACTGGGGCAAAAAAATTATCCTCTATATTCCCCCAAAATTACCAATATGATACTG
                                                                                                                                                                                 Unknow...
Unclassified.
Unclassified.
1 (bases 1 to 2794)
1 (bases 1, Redmond, M. J. and Hughes, H.P.A.
Potter, A.A., Redmond, M. J. and Hughes, H.P.A.
Enhanced immunogenicity using leukotoxin chimeras
Patent: US 5422110-A 1 06-JUN-1995;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                     Unknown.
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                                                                                                                                                                                                                                                                                                                                                                                       I12257
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                                                                                             Conservative
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487 c 599 g
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                                                                                         Score 814.4; DB 6;
Pred. No. 6.2e-133;
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US 5422110.
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1243	ctaaccgtttacaaggtaaaattttagagtgggaaaagcaaaatggcggtcagaactatt	1184	Qy	
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1183	acaggattgatctctggaattttagaagcgtctaaacaggcaatgtttgaaagt	$\vdash$	Qy	
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1036	CTATTGATGCATCGGTTACTGCAATTAATACCGCATTGGCCGCTATTGCTGGTGGT	977	рb	
1063	tactattgaagcttcattaactacaattagta	1004	у	
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856	GGCCTGTGGCTTTAATTGCTTCTACTGTTTCTCTTGCGATTAGCCCATTAG	797	Db	
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796	TTTTAGCCCAACGTGTTGCAGCAGGTTTATCTT	737	Дb	
823	gtaacaaaagcaatttcttcatatgttttagcacaacgtgttgctgctggtctatcaa	764	Qy	
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763	tgcatcgactggcaaaaaagttgctgcaggttttgaattaagcaatcaagttattggta	704	Qy	
676	AGATGTTATCTCAGGGCTATTATCGGGCGCAACAGCTGCACTTGTACTTGCAGATAAAA	617	DЬ	
703	aataattactggtttgctato	644	Qy	
616	AGGGACTTTAGGAGACAAACTCAAAAATATCGGTGGACTTGATAAAGCTGGCCTTGGTT	557	Db	
643	tataggaaacaagttgcaaaacttaaatttttctaaaacaaatcttggtt	587	Qy	
556	GACGAATTTGGTGAGCAAATTAGTCAATTTGGTTCAAAACTACAAAATATCAAAGGCT	497	Дb	
586	tgaagcattttcttcacagttagcaaagttaggttctactatatcgcaggctaaaggct	527	Qy	
496	GGAGCTAACAAATTCATTAATTGAAAAATATTGCTAATTCAGTAAAAAACAC	437	Db	
526	agctagtattgacttgattaatgagataattggtaatctatct	467	Qy	
436		380	DЪ	
466	gggtatagaacttgattctttaatcaaaaaaggtgatgctgcacctgatgctttggcta	407	Оу	
379	TGCAAATAAAGCCAAAACTGTATTATCTGGCATTCAATCTATTTTAGGCTCAGTATTGG	320	дь	
406	nagcaagtaatgtattatcaacattaagctcttttttgggcactgcattag	347	Qy	
319	AAACTAAAGCAGGCCAAGCATTAGGTTCTGCCGAAAGCATTGTACAAA	269	Db	
346	aaaacattctaccaataagttagccaaagggttagacagtgtagaaaatattgatcgta	287	Qy	
268	GTGTTATCCGCTCCACAAATTGATAAATTGCTAC	209	Db	
286	ctctctctcacacaaactggtattgctatttctgcaacaaaattagaaaagttcttac	227	Qy	
208	AAAGAGAAGAACGCAATAATATTGCAACAGCTCAAACCAGTTTAGGCACGATTCAAACCG	149	DЬ	
226	gcagaagagcctaatcacactgaaacagcaaaaaaatctgttgacacagtaaatcagt	167	Qy	
148	AACAAGGTAATGGTTTACAGGATTTAGTCAAAGCGGCCGAAGAGTTGGGGATTGAGGTAC	89	Db	

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                  gttctggtgatgatgtattaaatggtggtgctggtaatgatgtctatatctttcggaaag
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cgggtatagaacttgattctttaatcaaaaaaggtgatgctgcacctgatgctttggcta
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Potter,A.A. and Harland,R.J.
Haemophilus somnus outer membrane protein
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Patent: US 5534256-A 1 09-JUL-1996;
Location/Qualifiers
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tactt 1483       1456	1424 aagettatgeagatgettttgaagatggeaagaaagttgaagetggtteeaatatt 	Db Qy
ggaa 14       GGTA 13	364 ataataatattggtgagttagcaggtattaccaaattgggtgaacgcattaaga 	Фр
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	TCACCTCAAAGCAAGTTGATGATCTTAT 25	2528	Db
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2533	ttatcaaagtaataaaacagatcataaaattgagcaactaattggt	47	Qy ¦
6 7	atcattcaggtagtattaacataccaagatggtacataacatcaacat	2423	D Qy
2407	GAACTTAAAAGATTTAACATTTGAAAAAAGTTAAACATAATCTTGTCATCACGAA	. ω 5	) Db
- 4	aatatatctgatattatgattgaacgtaccaaagagggtattatagttaaacgaaaat	w	Qy
2350	GATGGTAATGATATTATTACCGATTCTGACGGCAATGATAAATTATCATTCTCTC	2291	Db
	gtgatggtaatgatactttgtacgatggcacgggcaatgataaattagcatttgcagatg	2303	Оу
2290	CAACGACCTATTACACGGTGGCAAGGGCGATGATATTTTCGTTCACCGTAAA	2231	dd .
2302	ttctggtgatgatgtattaaatggtggtgctggtaatgatgtctatatct	2243	Qy
2230	TTGGTGGTAAAGGCGATGATATTCTCGATGGTGGAAATGGTGATGATTTTATCGATGGCG	2171	Db
2242	gtggtaaaggcaacgatcgactt	2183	Qy
2170	AATGACCO	2111	Db
2182	tattccatagtggtgaaggtgatgatttactcgatggtggtggtggtggtgacgaccgcttgt	2123	Qy
2110	CATCACATAACGATATCTTTAAAGGTAGTAAGTTCAATC	2051	Db
2122	gaagaagtaattggttctcaatttaatgatgtattcaaa	2063	Qy
2050	AGCAATAACCAGCACCATGCCGGTTATTACACCAAAGATACCTTGAAAG	1994	Db
2062	tgattatgaattaagaaaagttgggtatggttatca	2003	Qy
1993	GACTTCAACCCATACCGCATTAGTGGGCAACCGTGAAGAAAAAATAGAATAT	1934	Дb
2002	gaagttgtgaagcgtcaagaaaccaaggtgggtaaacgtactgaaactat	1943	Qy
1933	AGAGACCGAGCAAGGTAGTTATACCGTAAATCGTTTCGTAGAAACCGGTAAAGCACTAC	1874	Db
1942	caacagaagcaggcagttatacagttaatcgtaaggttgctcgaggtgatatct	1883	Qy
1873	NCTATAGCCGTGGAAACTATGGTGCTTTAACTATTGATGCAACC	1817	Db
1882	gatcgtgtcttctatagtaaagacggaggatttggtaatattactgtagatggtac	1823	QУ
1816	AAGGTGATGACAACGTATTTGTTGGTTCTGGTACGACGGAAATTGATGGCGGGTGAAGGTT	1757	Db
1822	atgacgatatctttgttggtcaaggtaaaatgaatattgatggtggagatggac	1763	Qу
1756	AATGTAACTAAAACCAAAGAAAACAAAAATTATTGCCAAACTTGGTG	1697	Db
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1696	TTCAGCGTATTGGTATTGAAT	1637	Db
1723	gagaggctagttctaaattagatttctctaaagttattcagcgtgtagccgagacag	1664	Оу
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1663	aaatactcttatattaataagttaaaattcggacgtgtaaaaaaactggcaagttacag	1604	Qy
1576		1517	Db
1603	gcatttcacttcgcctttgttaacagcaggaactgaatcacgtgaacgtttaactaatg	1544	Qy
1516	TGGATTCGGCAAACGGTATTATTGATGTGAGTAATTCGGGTAAAGCGAAAACTCAGCATA	1457	Db

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Potter,A.A., Redmond,M.J. and Hughes,H.P.
Enhanced immunogenicity using leukotoxin
Patent: US 5708155-A 1 13-JAN-1998;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unknown.
Unclassified
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Sequence
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Potter,A.A. and Manns,J.G.
GnRH-leukotoxin chimeras
Patent: US 5723129-A 5 03-MAR-1998;
Location/Qualifiers
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gaagaagtaattggtt                 GAAGAAATTATCGGTA	gattatgaattaagaa    CATAGCAATAACCAGC	gaagttgtgaagcgtc        GAAGTGACTTCAACCC	gcaacagaagcaggcag                        GAGACCGAGCAAGGTAG	gatcgtgtcttctata                    GACCGAGTTCACTATA	gcaatgacgatatct              GTGATGACAACGTAT	gcacagacgagattg 	ggagaggctagttcta 	AAATATGAATATATTA	catttcacttcgcctt                 TTATTCAGAACGCCAT	gatgctaaaactggta                    ATTCGGCAAACGGTA	gettatgeagatgett                  GCCTATGTGGATGCGT	aataatattggtgagt                 AACAACATTGGTGATT	gagctaaataaagagt                AACTTAAACAAAGAGT	gataaaggctatgatt                GAAAATGGTTACGATG	taaccgtttacaaggta                AAATAAAATTCATAACA	acaggattgatctctgg:                ACCGGTGTAATTTCTAC	teegetgetgetgtage                   TCTGCTGCTGCAGCCG
.ctcaatttaatgatgt                  CATCACATAACGATAT	aagttgggtatggtta 	aagaaaccaaggtggg               ATACCGCATTAGTGGG	gttatacagttaatcg          TTATACCGTAAATCG	gtaaagacggaggatt            CCGTGGAAACTA	ttgttggtcaaggtaa         TTGTTGGTTCTGGTAC	gtctaatagtaaatgc 	AATTAGATTTCTCTAA 	agttaaa         AGCTCAA	tgttaacagcaggaac                  TATTGACGCCGGGAAC	tcatagacattagtaa                  TTATTGATGTGAGTAA	ttgaagatggcaagaa                 TTGAAGAAGGCAAACA	tagcaggtattaccaa               TAGCTGGTATTAGCCG	tggaagctgaacgtgt                 TACAGGCAGAACGTGT	ctcgttatgctgctta                 CCCGTTATCTTGCGAA	.aaaattttagagtggga                    AAAATTGTAGAATGGGA	gaattttagaagcgtc          CGATTCTGCAATATTC	gatctgctgttggtgc                   GCTCGGTTATTGCTTC
tattcaaaggttctaa              CTTTAAAGGTAGTAA	atcagtctaccgataa 	gtaaacgtactgaaac                CAACCGTGAAGAAAA	ytaaggttgctcgagg 	Ltggtaatattactgt              ATGGTGCTTTAACTAT	aaatgaatattgatgg 	caaaa       AACAAAAATTATTGC	aagttattcagcgtgt                 ACGTTGTTCAGCGTAT	yacgtgtaaaaaactg              	otgaatcacgtgaacg                  CAGAGCATCGTGAACG	attcaaatgggaaaaaa       TTCGGGTAAAGCGAAA	agttgaagctggt              CATTAAAGCCGAT	TT - t	ttattgcaatcaccca                   CATCGCTATTACTCA	atttagctaataactt        TTTACAAGATAATAT	haaagcaaaatggcgg                hAAAAAATAATCACGG	Ctaaacaggcaatgtt           TAAACAAGCAATGTT	caccgattgcactatt            ACCGATTGCCTTATT
aattcaacgaca            AGTTCAATGATG	atttgaaatcag              CCTTGAAAGCTG	statccagtatc            AATAGAATATC	gtgatatctacc 	tagatggtacga             TGATGCAACCA	Jtggagatggac             CGGTGAAGGTT	CCAAACTTGGTG	tagccgagacag 	ygcaagttacag               GAAAATTACAG	Jtttaactaatg           GCTACAAACAG	aaacgcaagcgt          AAACTCAGCATA	caatattact   ATTAGTACAG	ctaagagcggaa             	aacaacgttggg             AGCAGCAATGGG	caaaattttgt             GAAATTCTTAC	ytcagaactatt              TAAGAACTACT	tgaaagtgttg            TGAGCACGTTG	cagttgcaggtg           raGTATCTGGGA
2122 2110	2062 2050	2002 1993	1942 1933	1882 1873	1822 1816	1762 1756	1723 1696	1663 1636	1603 1576	1543 1516	1483 1456	1423 1396	1363 1336	1303 1276	1243 1216	1183 1156	1123 1096

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tattccatagtggtgaaggtgatgatttactcgatggtggtgctggtgacgaccgcttgt 2182
                      TGCCTAATTATAAAGCAACTAAAGATGAGAAAATCGAAGAAATCATCGGTCAAAATGGCG 2527
                            ----ttatcaaagtaataaaacagatcataaaattgagcaactaattggtaaagatggta
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Search completed: September 15, 2002, 11:15:40 Job time: 25125 sec

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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SPTREMBL_19:*

Sp_bacteria

sp_bacteria

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sp_fungi:*

Sp_fungi:*

sp_human:*

sp_human:*

sp_manma?

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rsp_manma.

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sp_phage:*
sp_plant:*
sp_plant:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
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sp_archeap:*
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sp_mammal:*
sp_mhc:*
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sp_bacteria:*
SUMMARIES
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Result No.	Score	% Query Match	Length	DB	ID	Description	tion
_	57	100.0	927	2	Q93GI2	Q93gi2 п	moraxella b
2	43	75.4	946	N	Q9EV24	Q9ev24 m	mannheimia
ω	43	75.4	953	N	Q9ETX2	Q9etx2 п	mannheimia
4	43	75.4	953	N	Q9ETG5	Q9etg5 p	pasteurella
υ	43	75.4	953	N	Q9EV34		pasteurella
0	43	75.4	953	N	Q9EV33	Q9ev33 p	pasteurella
7	43	75.4	953	N	Q9EV32	Q9ev32 p	pasteurella
8	43	75.4	953	N	Q9EV31	Q9ev31 p	pasteurella
9	43	75.4	953	N	Q9EV30	Q9ev30 p	pasteurella
10	43	75.4	953	N	Q9EV29	Q9ev29 p	pasteurella
11	43	75.4	953	N	Q9EV27	Q9ev27 p	pasteurella
12	43	75.4	953	N	Q9EV26	Q9ev26 п	mannheimia
13	43	75.4	953	N	Q9EV25	Q9ev25 п	mannheimia
14	43	75.4	953	N	Q9EV23	Q9ev23 п	mannheimia
15	43	75.4	953	N	Q9EV28	Q9ev28 p	pasteurella
16	43	75.4	2	د	0951153		224

44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
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088651 marmota mon 004767 bolusanthus	O80380 daucus caro	Q9w4n7 drosophila	Q28298 canis famil	N	Q9qym7 cricetulus		Q9rjkO streptomyce	Q63779 rattus norv	rat		Q96sb2 homo sapien	ente		homo	0	O25891 helicobacte		O80148 bacteriopha	Q932b3 staphylococ		Q9mbs7 staphylococ	Q90307 carassius a		013098 xenopus lae	Q93np1 actinobacil	Q9ev22 pasteurella	Q9eud4 pasteurella

# ALIGNMENTS

RESULT Q9EV24 ID Q AC Q DT 0 DT 0	Qy Ma Qy	SO RECEIVED TO SO	RESULT Q93GI2 ID Q AC Q DT 0
LT 2  724  724  PRELIMINARY; PRT; 946 AA.  Q9EV24;  Q1-MAR-2001 (TrEMBLrel. 16, Created)  O1-MAR-2001 (TrEMBLrel. 16, Last sequence update)  O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)	Query Match 100.0%; Score 57; DB 2; Length 927; Best Local Similarity 100.0%; Pred. No. 0.17; Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  1 FLSELNKELEAE 12	(TEMBLIEL 19, Last (TEMBLIEL 19, Last vois roteobacteria; gamma: 476; 476; 476; 476; 476; 476; 476; 476;	1 93GI2 PRELIMINARY; 93GI2; 1-DEC-2001 (TrembLrel.)

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Best Local S
Matches
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Best Local :
                                                                                                                              STRAIN=PH498, AND PH344;

Davies R.L., Whittam T.S., Selander R.K.;

"Sequence diversity and molecular evolution of the gene in bovine and ovine strains of Mannheimia (Pa haemolytica.";

J. Bacteriol. 0:0-0(2001).

EMBL; AF314518; AAG40302.1; -.

EMBL; AF314517; AAG40301.1; -.

EMBL; AF314517; AAG40301.1; -.

InterPro; IPR001753; Enoyl_CoA_hydrtse.

InterPro; IPR001343; Hemlysn_Ca_bind.

InterPro; IPR003355; RTX_N.

Pfam; PF00353; hemolysinCabind; 1.

Pfam; PF00382; RTX; 1.
                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                 Q9ETX2;
Q9ETX2;
01-MAR-2001
01-MAR-2001
01-JUN-2001
                                                                                                          PRINTS; F
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0313; CABNDNGRPT.
PROSITE; PS00166; ENOYL_COA_HY
SEQUENCE 946 AA; 101480 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF314521; AAG40305.1; -.
InterPro; IPR001753; Enoyl_CoA_hydrtse.
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR003355; RTX_N.
Pfam; PF00353; hemolysinCabind; 1.
Pfam; PF02382; RTX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-PH574;
MEDLINE-21101823; PubMed-11157953;
Davies R.L., Whittam T.S., Selander R.K.;
"Sequence Diversity and Molecular Evolution of "Sequence Diversity and Molecular Evolution of Mannheimia"
                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                  Mannheimia glucosida.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                            LKTA
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Bacteria; Proteobacteria;
Mannheimia.
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                                                                                                                                                                                                                                                                                                                          Mannheimia
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                                               Local
              1 FLSELNKELEAE
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                                                                                         PR00313; CABNDNGRPT.
;; P800166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
E 953 AA; 102135 MW; 70DB354157F5881E
                                    h 75.4%;
Similarity 75.0%;
9; Conservative
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9; Conser
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75.0%;
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                                                                                                                                                                                                                                                                                                                                 gamma
                                   Score 43; DB Pred. No. 45; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                             Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _HYDRATASE; UNKNOWN_1
MW; 25C077858BDC76C4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 43; DB
Pred. No. 45;
1; Mismatches
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                                      2;
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                                                          Length 953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 946
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(Pasteurella)
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                                   Gaps
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RESULT
Q9EV34
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Best Local
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01-MAR-2001
01-JUN-2001
                                                                                                                                                                                                                                 Q9EV34;
Q9EV34;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
SEQUENCE
J. Bacteriol. 183:1394-1404(2001).
EMBL; AF314505; AAG40289.1; -
InterPro; IPR001753; Encyl_CoA_hydrtse.
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR003355; RTX_N.
                                                                MEDLINE-21101823; PubMed-11157953;
Davies R.L., Whittam T.S., Selander R.K.;
"Sequence Diversity and Molecular Evolution of
Gene in Bovine and Ovine Strains of Mannheimia
                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Bacteriol. 0:0-0(2001).

EMBL: AF314507; AAG402991.1; -.

EMBL: AF314504; AAG402881.1; -.

EMBL: AF314506; AAG40290.1; -.

Interpro; IPR001753; Enoy1_Co_hydrtse.

Interpro; IPR001743; Hemlysn_Ca_bind.

Interpro; IPR003355; RTX_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=PH284, PH388, AND PH8;
Davies R.L., Whittam T.S., Selander R.K.;
"Sequence diversity and molecular evolution of
                                                                                                                                                                 Pasteurella haemolytica.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00353; hemolysinCabind; Pfam; PF02382; RTX; 1. PRINTS; PR00313; CABNDNGRPT.
                                                                                                              STRAIN-PH56
                                                                                                                                                                                                            01-MAR-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene in bovine and ovine strains of Mannheimia
haemolytica.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria;
Mannheimia.
                                                        haemolytica.";
                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                             NCBI_TaxID=75985;
                                                                                                                                                         Mannheimia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=75985;
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Similarity 75.0%;
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
953 AA; 101997 MW; D593D6A577C3ADE9
                                                                                                                                                                                                           (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
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PH388,
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1; Mismatches
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J. Bacteriol. 183:1394-1404(2001).

EMBL; AF314508; AAG40292.1; -.

InterPro; IPR001753; Enoyl_CoA_hydrt
InterPro; IPR001353; Hemlysn_Ca_bind
InterPro; IPR003353; RTX_N.

Pfam; PF00353; hemolysinCabind; 1.
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Pfam; PF02382; RTX;
PRINTS; PR00313; CABB
PROSITE; PS00166; EN
SEQUENCE 953 AA;
                                                                                                                                                                                                                                             Q9EV32;
Q9EV32;
Q1-MAR-2001;
Q1-MAR-2001;
Q1-DEC-2001;
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01-DEC-2001
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Pfam; PF02382; RTX; 1.
PRINTS; PR00313; CABNDWGRPT.
PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
SEQUENCE 953 AA; 102010 MW; DE48B28EE0EB09FB CRC64;
                                                                                                                                                                                        LKTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-21101823; PubMed-11157953;
Davies R.L., Whittam T.S., Selander R.K.;
"Sequence Diversity and Molecular Evolution of the Leukotoxin
Gene in Bovine and Ovine Strains of Mannheimia (Pasteurella)
                                                                                                                      Pasteurella haemolytica.
Bacteria: Proteobacteria;
                                                                                                                                                                                                                      LEUKOTOXIN.
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SEQUENCE FROM N.A.
                                                           NCBI_TaxID=75985;
                                                                                            Mannheimia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=75985;
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75.0%;
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Hemlysn_Ca_bind.
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Pred. No.
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01-MAR-2001
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EMBL; AF314509; AAG40293.1; -
InterPro; IPR001753; Emoyl_Coa_hydrtse.
InterPro; IPR001343; Hemlysn_Coa_bind.
InterPro; IPR003355; RTX_N.
Ffam; PF00353; hemolysinCabind; 1.
Pfam; PF002382; RTX; 1.
PPINTS; PR00313; CABNDMGRPT.
PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
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EMBL; AF314510; AAG40294.1; ...
InterPro; IPR001753; Enoyl_Coa_hydrtse.
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR003355; RTX_N.
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"Sequence Diversity and Molecular Evolution of the Leukotoxin (lkta)
Gene in Bovine and Ovine Strains of Mannheimia (Pasteurella)
haemolytica.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21101823; PubMed=11157953; Davies R.L., Whittam T.S., Selander R.K.; Sequence Diversity and Molecular Evolution Gene in Bovine and Ovine Strains of Mannheim haemolytica.";
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Bacteria; Proteobacteria;
                                                                                                                                                                                                                     PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
SEQUENCE 953 AA; 102160 MW; A189BF80754A7907
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                                                                                               Conservative
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Best Local
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EMBL; AF314514; AAG40298.1; -
InterPro; IPR001753; Enoyl_CoA_hydrtse.
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR003355; RTX_N.

Pfam; PF00353; hemolysinCabind; 1.
Pfam; PF02382; RTX; 1.
Pfam; PF02382; RTX; 1.
PRINTS; PR00313; CABLUNGRPT.
PROSITE; PS00166; ENOYL_COA_HYDRATASE; UN
SEQUENCE 953 AA; 102147 MW; 11600FDA7
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Q9EV29;
Q1-MAR-2001
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MEDLINE=21101823; PubMed=11157953;
Davies R.L., Whittam T.S., Selande
Davies R.L., Whittam T.S., Selande
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Mannheimia.
                                                                                                                                                                                                                                                                                                                     Gene
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Pacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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MW; 4E8F11490479A69A CRC64;
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MEDLINE=21101823; PubMed=11157953;
Davies R.L., Whittam T.S., Selander R.
"Sequence Diversity and Molecular Evol
Gene in Bovine and Ovine Strains of Ma
haemolytica.";
J. Bacteriol. 183:1394-1404(2001).
EMBL; AF314519; AAG40303.1; -
InterPro; IPR001753; Enoyl_CoA_hydrtse
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Bacteria; Proteobacto
Mannheimia.
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InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR001355; RTX_N.
Pfam; PF00353; hemolysinCabind; 1.
Pfam; PF00382; RTX; 1.
PFANT; PF00382; RTX; 1.
PRINTS; PR00313; CABNDNGRPT.
PROSTTE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN 1.
SEQUENCE 953 AA; 102230 MW; 2B686808EB370090
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Mannheimia.
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EMBL; AF314516; AAG40300.1; -.
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9; Conser
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                                                                                                                                                                                                                                                                       Proteobacteria;
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Enoyl_CoA_hydrtse
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lecular Evolution of
trains of Mannheimia
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Last sequences
Last anno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                     subdivision; Pasteurellaceae;
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                                                                               ler R.K.;
c Evolution of
of Mannheimia
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(Pasteurella)
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(Pasteurella)
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Best Local
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Best Local :
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09EV23;
01-MAR-2001
01-MAR-2001
01-DEC-2001
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01-MAR-2001
01-MAR-2001
01-DEC-2001
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Pfam; PF02382; RTX; 1.
PRINTS; PR00318; CABNDWGRPT.
PROSITE; PR00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
SEQUENCE 953 AA; 102236 MW; AC5874B3B75D1C98 CRC64;
                           Mannheimia glucosida.
Bacteria; Proteobacteria;
Mannheimia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO0313; CABNDNGRPT.

PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.

SEQUENCE 953 AA; 102138 MW; C41D9EBC1D799951 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF314520; AAG40304.1; InterPro; IPR001753; Enoyl_CoA_hydrtse. InterPro; IPR001343; Hemlysn_Ca_bind. InterPro; IPR003355; RTX_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21101823; PubMed=11157953;
Davies R.L., Whittam T.S., Selander R.K.;
"Sequence Diversity and Molecular Evolution
Gene in Bovine and Ovine Strains of Mannheim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mannheimia glucosida.
Bacteria; Proteobacteria;
                                                                                                                                                    LEUKOTOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Bacteriol. 183:1394-1404(2001).
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InterPro; IPR003355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              451
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nes 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                             FLLNLNKELQAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF00353; hemolysinCabind; PF02382; RTX; 1.
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9; Conserv
                                                                                                                                                                            (TrEMBLrel. 16, (TrEMBLrel. 16, (TrEMBLrel. 19,
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                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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75.0%;
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19,
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Last annotation update)
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                                                                                                                                                                            Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
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                                                               subdivision;
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Mannheimia
                                                                                                                                                                                                                                                                                                  953
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                                                               Pasteurellaceae;
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Query Match
Best Local Similarity
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QPEV28
ID EV28
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ID O1
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Q9EV28;
01-MAR-2001
01-MAR-2001
01-DEC-2001
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SEQUENCE FROM
STRAIN-PH290;
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InterPro; IPR001753; Enoyl_CoA_hydrtse.
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR001335; RTX_N.
Pfam; PF00353; hemolysinCabind; 1.
Pfam; PF00353; hemolysinCabind; 1.
PRO3352; RTX; 1.
PRINTS; PR00313; CABNUMGRPT.
PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
PROSITE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
                                                                                                                 Davies R.L., Campbell S., Whittam T.S.;

"Mosaic structure and molecular evolution of the leukotoxin of
(lktCABD) of Mannheimia (pasteurella) haemolytica, Mannheimia
glucosida and Pasteurella trehalosi.";
J. Bacteriol. 0:0-0(2001).
EMBL; AR914515; AA640299.1; -.
EMBL; AR914611; AAL13281.1; -.
EMBL; AR914141; AAL13281.1; -.
EMBL; AR914141; AAL13281.1; -.
EMBL; AR914141; AAL13281.1; -.
EMBL; AR914515; AFOYL COA hydrtse.
InterPro; IPR001353; Emoyl CoA hydrtse.
InterPro; IPR003355; RTX_N.
Pfam: PR00353; hemolysinCabind; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-PH292, AND PH296;
MEDLINB-21101823; PubMed-11157953;
Davies R.L., Whittam T.S., Selander R.K.;
"Sequence Diversity and Molecular Evoluti
Gene in Bovine and Ovine Strains of Mannh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-21101823; PubMed-11157953; Davies R.L., Whittam T.S., Selander R.K.; Pavies R.L., Whittam T.S., Selander R.K.; Selander Boolution of the Leukotoxin (lkta) "Sequence Diversity and Molecular Evolution of the Leukotoxin (lkta) Gene in Bovine and Ovine Strains of Mannheimia (Pasteurella)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pasteurella haemolytica.
Bacteria; Proteobacteria;
Pfam; PF02382; RTX; 1.
PRINTS; PR00313; CABNDNGRPT.
PROSTIE; PS00166; ENOYL_COA_HYDRATASE; UNKNOWN_1.
SEQUENCE 953 AA; 102218 MW; 04AB1715B819E571 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-PH296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEUKOTOXIN (LKTA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Bacteriol. 183:1394-1404(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  haemolytica."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=75985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mannheimia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             haemolytica."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             451 FLLNLNKELQAE 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
nes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 FLSELNKELEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteriol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 16, (TrEMBLrel. 16, (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183:1394-1404(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75.4%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecular Evolution of Strains of Mannheimia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Pasteurella)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the Leukotoxin (1ktA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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75.4%; 75.0%;

Score Pred.

No.;

DB 45;

ν,

Length 953;

Page 6

Db Search completed: September 11, 2002, 09:01:26 Job time: 284 sec Matches 1 FLSELNKELEAE 12 || |||||:|| 451 FLLNLNKELQAE 462 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

RESULT 1 AAF57290 ID AAF57290 standard; DNA; 3231 BP

Moraxella; antigen; immune response; infection; RTX toxin; vaccine; antibacterial; ds. 29-MAY-2001 (first entry) AAF57290; Key CDS M. bovis Dalton 2d RTX toxin A subunit encoding DNA. CDS Moraxella bovis. Location/Qualifiers 232..3015 /\*tag= b 'note= "partial coding region of RTX toxin C subunit" 1080..3250 rtag= a product= "RTX toxin A subunit"

WO200116172-A1.

08-MAR-2001.

31-AUG-2000; 2000WO-AU01048.

CDS

/note- "partial coding region of RTX toxin B subunit"

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RESULT
AAB62110
                                                                                                                                                          SXX CCCCCCCXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB62110 standard; Protein; 927 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Moraxella; antigen; immune response; infection; RTX toxin; vaccine; antibacterial; A subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB62110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M. bovis Dalton 2d RTX toxin A subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200116172-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Moraxella bovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-AUG-2000; 2000WO-AU01048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-MAR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-AUG-1999;
                                                              100.0%; Score 77; DB 22; Length 927; Query Match 100.0%; Pred. NO. 7.4e-05; Best Local Similarity 100.0%; Pred. No. 7.4e-0; Indels 0; Matches 14; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                farn J, Strugnell R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CSIR ) COMMONWEALTH SCI & IND RES ORG. (UYME ) UNIV MELBOURNE.
                                                                                                                                                                                                                                                                                                                                                                                      Novel Moraxella bovis antigen useful in compositions for raising immune response in an animal, has protease, lipase or hemolysin activity
                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAF57290.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-235092/24.
                                                                                                                                                                                        The invention relates to new Moraxella bovis antigens and nucleic acid sequences encoding these antigenic polypeptides. The antigenic sequences encoding these antigenic sequences encoding these antigenic response in an animal directed against Moraxella, preferably against response in an animal directed against Moraxella infections. The M. bovis or M. catarrhalls, and for treating Moraxella infections. The present sequence represents the amino acid sequence of the A subunit of the RTX toxin from M. bovis Dalton 2d.
                                                                                                                                                                                                                                                                                                                                         Claim 26; Fig 5; 60pp; English.
                                                                                                                                                            Sequence
1 FNDIFHSGEGDDLL 14
||||||||||||||
| 705 fndifhsgegddll 718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99AU-0002571.
                                                                                                                                                                       927 AA;
                                                                                                             0; Gaps
                                                                                                                        .
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#### ALIGNMENTS

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SEQ 6
AAB62110
ID
     AAB62110 standard; Protein; 927 AA.
хx
     AAB62110;
ХX
DT
     29-MAY-2001 (first entry)
XX
     M. bovis Dalton 2d RTX toxin A subunit.
ХX
     Moraxella; antigen; immune response; infection; RTX toxin; N
KW
XX
     antibacterial; A subunit.
     Moraxella bovis.
XX
PN
     WO200116172-A1.
XX
PD
XX
     08-MAR-2001.
     31-AUG-2000; 2000WO-AU01048.
XX
PR
     31-AUG-1999;
                   99AU-0002571.
ХΧ
     (CSIR ) COMMONWEALTH SCI & IND RES ORG.
PA
     (UYME ) UNIV MELBOURNE.
ΧX
ΡI
     Farn J, Strugnell R, Tennent J;
ХX
DR
     WPI; 2001-235092/24.
     N-PSDB; AAF57290.
ХX
     Novel Moraxella bovis antigen useful in compositions for raising immune
PΤ
     response in an animal, has protease, lipase or hemolysin activity
       Claim 26; Fig 5; 60pp; English.
       The invention relates to new Moraxella bovis antigens and nucleic acid
  CC
```

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The invention relates to new Moraxella bovis antigens and nucleic acid sequences encoding these antigenic polypeptides. The antigenic polypeptides and polynucleotides are useful for raising an immune response in an animal directed against Moraxella, preferably against M. bovis or M. catarrhalis, and for treating Moraxella infections. The present sequence represents the amino acid sequence of the A subunit of the RTX toxin from M. bovis Dalton 2d.
CC
CC
XX
                          Sequence 927 AA;
```

100.0%; Score 57; DB 22; Length 927; 100.0%; Pred. No. 0.2; tive 0; Mismatches 0; Indels Query Match Best Local Similarity 100 Matches 12; Conservative

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1 FLSELNKELEAE 12
Qy
   Db
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RESULT

·88 ·

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RESULT
AAR86998
        AAR86998 standard; Protein; 758 AA.
ХX
        AAR86998;
        04-JUL-1996 (first entry)
DT
XX
        Enterohaemorrhagic E.coli hlyA gene product.
        Enterohaemorrhagic Escherichia coli; virulent; EHEC; 0157:H7 serotype;
ХΧ
KW
KW
        detection; probe; primer; hlyA gene; enterohaemorrhagic colitis; haemolytic uremic syndrome; mesenteric adenitis.
KW
XX
         Escherichia coli (enterohaemorrhagic).
os
        US5475098-A.
PN
ХX
         12-DEC-1995.
XX
                                    94US-0258188.
PF
         14-JUN-1994;
         14-JUN-1994;
                                    94US-0258188.
PR
XX
         (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI
         Hall RH, Xu JG;
XX
DR
         WPI; 1996-048546/05.
N-PSDB; AAT08098.
 DR
         Entero:haemorrhagic E. coli (EHEC) nucleic acid sequences - useful for probe and primer design for sensitive and specific detection of EHEC
XX
PT
PT XX PS XX CC CC CC CC CC
         Claim 1; Columns 37-42; 32pp; English.
         Enterohaemorrhagic E.coli (EHEC) associated with enterohaemorrhagic colitis, haemolytic uremic syndrome and mesenteric adenitis have been found to carry a hlyA gene and a hylB gene, separated by an intergenic region. The hly genes and the intergenic region are absent from bacteria not associated with these diseases and so provide a useful target for detecting EHEC pathogens, esp. 0157:H7 serotype E.coli. The present sequence is that of the protein encoded by the EHEC hlyA gene.
 CC
                             758 AA;
          Sequence
                                                67.5%; Score 52; DB 17; Length 758; 57.1%; Pred. No. 1.4; tive 3; Mismatches 3; Indels
     Best Local Similarity
                                                                                                                      0; Gaps
                         8; Conservative
                1 FNDIFHSGEGDDLL 14
  Qу
             |||||| :|:| :
480 fndifhgadgndyi 493
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RESULT
AAW22159
ID
           AAW22159 standard; Protein; 1049 AA.
ХX
           AAW22159;
           16-FEB-1998 (first entry)
DT
DE
           ApxIIIB protein.
ХX
           RTX toxin; apxICA gene; apxIBD gene; apxIIAB'C gene; apxIIIABCD gene; repeat in toxins toxin; cell-associated RTX toxin; vaccine production; therapy; A. pleuropneumoniae infection; swine pleuropneumonia.
KW
os
            Actinobacillus pleuropneumoniae.
ХX
            CA2170839-A.
XX
PD
            02-SEP-1996.
                                               96CA-2170839.
            01-MAR-1996:
ХX
            01-MAR-1995;
                                               95US-0396244.
XX
PA
            (UYGU-) UNIV GUELPH.
           MacInnes J, Mallard B, Ricciatti P, Rosendal S;
PΙ
            WPI: 1997-245536/23
DR
            N-PSDB; AAT73220.
DR
           Preparations of microorganisms producing cell-associated RTX toxins - especially for production of vaccines against swine
PT
XX
PS
            pleuro-pneumonia
            Disclosure; Pages 107-110; 151pp; English.
XX
            AAW22151-W22161 represent A. pleuropneumoniae RTX (repeat in toxins)
           toxins. These sequence are encoded by the apxICA, apxIBD, apxIIAB'C, and apxIIIABCD genes (see AAT73217-T73220), and can be expressed by microorganisms used in the preparations of the invention. The preparations are bacterial preparations comprising one or more isolated
           preparations are bacterial preparations comprising one or more isolated and purified strains of a microorganism that produces one or more RTX toxins, where the strains have at least one cell-associated RTX toxin. The preparations are used for production of vaccines for the prophylaxis and treatment of infectious diseases caused by microorganisms that produce RTX toxins, where the strains have been attenuated or inactivated. The vaccines are preferably against Actinobacillus pleuropneumoniae infection (swine pleuropneumonia). It has been found that A. pleuropneumonia produces significant quantities of cell-associated RTX toxins when cultured under certain conditions, and
           that the whole-cell protein composition of the cultures corresponds to the whole-cell protein profiles obtained from cells recovered at necropsy from the pleural fluid of infected swine. Vaccination with a bacterin prepared from heat-inactivated cultures having significant quantities of cell-associated RTX toxins give significant protection of swine against challenge with homologous strains.
CC
 CC
             Sequence 1049 AA;
                                                               75.3%; Score 58; DB 18; Length 1049;
71.4%; Pred. No. 0.18;
tive 1; Mismatches 3; Indels
       Query Match
                                                                                                                                                             0; Gaps
       Best Local Similarity
                             10: Conservative
                      1 FNDIFHSGEGDDLL 14
  Qy
                 747 frdifhgadgddll 760
```

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2812

2992 ggaattttggctccaagtgtttag 3015

2528

741 ggtctaatagtaaatgcaaaagctggcaatgacgatatctttgttggtcaaggtaaaatg 1800 ggtctaatagtaaatgcaaaagctggcaatgacgatatctttgttggtcaaggtaaaatg 2031 aatattgatggtggagatggacacgatcgtgtcttctatagtaaagacggaggatttggt 1860 032 aatattgatggtggagatggacacgatcgtgtcttctatagtaaagacggaggatttggt 2091 gttgctcgaggtgatatctaccatgaagttgtgaagcgtcaagaaaccaaggtgggtaaa 1980 gttgctcgaggtgatatctaccatgaagttgtgaagcgtcaagaaaccaaggtgggtaaa 2211 cgtactgaaactatccagtatcgtgattatgaattaagaaaagttgggtatggttatcag 2040 cgtactgaaactatccagtatcgtgattatgaattaagaaaagttgggtatggttatcag 2271 tctaccgataatttgaaatcagtagaagaagtaattggttctcaatttaatgatgtattc 2100 tctaccgataatttgaaatcagtagaagaagtaattggttctcaatttaatgatgtattc 2331 aaaggttctaaattcaacgacatattccatagtggtgaaggtgatgatttactcgatggt 2160 ggtgctggtgacgaccgcttgtttggtggtaaaggcaacgatcgactttctggagatgaa 2220 ggtgctggtgacgaccgcttgtttggtggtaaaggcaacgatcgactttctggagatgaa 2451 ggcgatgatttactcgatggcggttctggtgatgatgtattaaatggtggtgctggtaat 2280 ggcgatgatttactcgatggcggttctggtgatgatgtattaaatggtggtgctggtaat 2511 2341 gataaattagcatttgcagatgcaaatatatctgatattatgattgaacgtaccaaagag 2400 2572 gataaattagcatttgcagatgcaaatatatctgatattatgattgaacgtaccaaagag 2631 ggtattatagttaaacgaaatgatcattcaggtagtattaacataccaagatggtacata 2460 ggtattatagttaaacgaaatgatcattcaggtagtattaacataccaagatggtacata 2691 ggtaaagatggtagttatatcacttccgatcaaattgataaaattttgcaagataagaaa 2580 2752 ggtaaagatggtagttatatcacttccgatcaaattgataaaattttgcaagataagaaa 2811 aaattatetgetteggacattgcaagtagettaaataagetagttgggteaatggcacta 2700 2872 aaattatctgcttcggacattgcaagtagcttaaataagctagttgggtcaatggcacta 2931 ggaattttggctccaagtgtttag 2784 [[[]]]]]][[[]]]

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Sep

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RESULT
AAQ10727
    AAQ10727 standard; DNA; 2788 BP.
XX
       AAQ10727;
AC
       11-APR-1991 (first entry)
DT
       Leukotoxin 352 gene in plasmid pAA352.
XX
       LKT; vaccine; antigen; respiratory disease; shipping fever pneumonia;
XX
KW
 KW
        Pasteurella haemolytica Al strain B122.
 os
 хх
        CA2014033-A.
 PN
 ХX
        07-OCT-1990.
 PD
                              90CA-2014033.
        06-APR-1990;
 PF
 XX
                              89US-0335018.
        07-APR-1989;
  ХX
         (UYSA-) UNIV SASKATCHEWAN.
         Acres SD, Babiuk LA, Potter AA, Lawman MJP;
  XX
PI
         WPI; 1991-000097/01.
  DR
         P-PSDB; AAR10889
  DR
         Pasteurella haemolytica proteins and genes - used for producing vaccines to protect animals esp. cattle from respiratory diseases
  PT
         e.g. pneumonia.
   PT
XX
PS
         Claim 13; Fig 5; 87pp; English.
          Plasmid pAA352 is derived from pAA114, a clone isolated from a genomic library of P. haemolytica. The protein encoded by the plasmid, "new leukotoxin" or "LKT 352" is 98% homologous to authentic leukotoxin. LKT 352 and pref. antigenic fragments of it, authentic leukotoxin. LKT 352 and pref. artigenic fragments of it, authentic leukotoxin. LKT 352 and pref. artigenic fragments of it, authentic leukotoxin. LKT 352 and pref. artigenic fragments of it, authentic leukotoxin. They can be used to protect cattle from respiratory diseases. They can also be used to produce antibodies for immunoaffinity purificn. of further proteins. [Fig. contg. sequence v. poor] purificn. of further proteins. [Fig. contg. sequence v. poor] See also AAR10890, AAR20909, AAR10910 and AAQ10783.
   CC
   CC
CC
   CC
           Sequence 2788 BP; 928 A; 487 C; 597 G; 776 T; 0 other;
       Query Match 29.4%; Score 817.6; DB 12; Length 2788; Best Local Similarity 60.0%; Pred. No. 3.5e-171; Matches 1530; Conservative 0; Mismatches 964; Indels 54;
              Qy
              DЪ
     Ov
              Db
     Qy
              Dр
      Qy
               Dþ
      Qy
       Db
               353 gtaaagcaagtaatgtattatcaacattaagctcttttttgggcactgcattagcgggta 412
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SEDIO
RESULT
AAR10889
        AAR10889 standard; Protein; 924 AA.
ID
XX
        AAR10889;
XX
DT
        11-APR-1991 (first entry)
XX
DE
        Leukotoxin 352 encoded by plasmid pAA352.
        LKT; vaccine; antigen; respiratory disease; shipping fever pneumonia.
KW
XX
         Pasteurella haemolytica Al strain B122.
XX
PN
         CA2014033-A.
         07-OCT-1990.
PΩ
                                   90CA-2014033.
         Q6-APR-1990;
             -APR-1989;
                                   89US-0335018.
           UYSA-) UNIV SASKATCHEWAN.
          cres SD, Babiuk LA, Potter AA, Lawman MJP;
         WPI; 1991-000097/01.
         N-PSDB; AAQ10272.
DR
ХX
        Pasteurella haemolytica proteins and genes - used for producing vaccines to protect animals esp. cattle from respiratory diseases
PT
PT
         e.g. pneumonia.
ХX
PS
         Claim 13; Fig 5; 87pp; English.
        Plasmid pAA352 is derived from pAA114, a clone isolated from a genomic library of P. haemolytica. The protein, designated "new leukotoxin" or "LKT 352" is 98% homologous to authentic leukotoxin. LKT 352 and pref. antigenic fragments of it, can be used in vaccines to protect cattle from respiratory diseases. They can, also be used to produce antibodies for immunoaffinity purificn. of further proteins. [Fig. contg. sequence v. poor]. See also AAR10890, AAR10909, AAR10910 and AAQ10783.
CC
         Sequence 924 AA;
        Query Match 63.6%; Score 49; DB 12; Length 924; Best Local Similarity 58.3%; Pred. No. 5.7; Matches 7; Conservative 3; Mismatches 2; Indels
                   2 NDIFHSGEGDDL 13
     Qy
                ||: | |:|||:
745 ndllhggkgddi 756
```

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```
RESULT
    leukotoxin A - Pasteurella haemolytica (serotype 1)
    C;Species: Pasteurella haemolytica (serotype 1)
C;Species: Pasteurella haemolytica
C;Date: 12-Oct-1989 #sequence_revision 15-Nov-1996 #text_change 18-Jun-1999
C;Accession: B30169; C32051; S29516
R;Highlander, S.K.; Chidambaram, M.; Engler, M.J.; Weinstock, G.M.
DNA 8, 15-28, 1989
    A;Title: DNA sequence of the Pasteurella haemolytica leukotoxin gene cluster.
    A; Reference number: A30169; MUID:89210283
A; Accession: B30169
    A; Status: not compared with conceptual translation
   A; Status: Not compared with conceptual translation
A; Molecule type: DNA-
A; Residues: 1-953 <HIG>
R; Strathdee, C.A.; Lo, R.Y.C.
J. Bacteriol. 171, 916-928, 1989
A; Title: Cloning, nucleotide sequence, and characterization of genes encoding the A; Reference number: A32051; MUID:89123172
A; Accession. C32051
    A; Accession: C32051
    A; Status: not compared with conceptual translation
   A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 947-953 <STR>
R; Lo, R.Y.C.; Strathdee, C.A.; Shewen, P.E.
Infect. Immun. 55, 1987-1996, 1987
    A:Title: Nucleotide sequence of the leukotoxin genes of Pasteurella haemolytica Al
   A; Reference number: S29515; MUID:87306837
    A; Accession: S29516
   A; Molecule type: DNA
A; Residues: 1-741,'D',743-953 <LOR>
A; Cross-references: EMBL: M20730; NID: g150492; PIDN: AAA25529.1; PID: g150494
   C; Comment: This organism causes bovine pneumonic pasteurellosis (shipping fever).
   C; Genetics:
   C; Function:
   A;Description: lyses leukocytes
C;Superfamily: hemolysin A; hemolysin A homology
  C;Superiamily: nemolysin A; nemolysin A nomology
C;Keywords: calcium binding; cytolysis; exotoxin; hemolysis; lipoprotein; tandem :
F;238-784/Domain: hemolysin A homology <HLYA>
F;716-807/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-{LVIYF]-X)
F;554/Binding site: palmitate (Lys) (covalent) #status predicted
      Query Match 50.0%; Score 2325; DB 1; Length 953;
Best Local Similarity 49.9%; Pred. No. 1.6e-111;
Matches 464; Conservative 175; Mismatches 264; Indels 2
                                                                                                                 26;
  Qy
                8 KSNIQAGLNSTKSGLKNLYLAIPKD--YDPQKGGTLNDFIKAADELGIARLAEEPNHTET 65
              Db
              66 AKKSVDTVNQFLSLTQTGIAISATKLEKFLQKHSTNKLAKGLDSVENIDRKLGKASNVLS 125
  Qy
              Db
  Qy
            126 TLSSFLGTALAGIELDSLIKKGDAAPDALAKASIDLINEIIGNLSQSTQTIEAFSSQLAK 185
            : | ||: |||::|| ::: ||||| ::| |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |:: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |
  Db
            Οv
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 Qy
            245 GFELSNQVIGNVTKAISSYVLAQRVAAGLSTTGAVAALITSSIMLAISPLAFMNAADKFN 304
           DЪ
           Qy
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           Qy
 Db
           425 AYLANNLKFLSELNKELEAERVIAITOORWDNNIGELAGITKLGERIKSGKAYADAFEDG 484
 Qy
           Db
           Qy
Db
Qy
           545 FGRVKNWQVTDGEASSKLDFSKVIQRV-----AETEGTDEIGLIVNAKAGNDDIFVGQ 597
           Db
          Qy
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          658 VGKRTETIQYRDYELRKVGYGYQSTDNLKSVEEVIGSQFNDVFKGSKFNDIFHSGEGDDL 717
Qy
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Qy
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Qy
          778 TGNDKLAFADANISDIMIERTKEGIIVKRNDHSGSINIPRWY----ITSNLQNYQSNKTD 833
          Db
Qу
          834 HKIEQLIGKDGSYITSDQIDKILQDKKDGTVITSQELKKLADENKSQKLSASDIASSLNK 893
```

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